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BG519751 602578902
BF311926 601897767
BQ69050 AGENCOURT
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BG335963 602739146
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Email: cgapbs-r@mail.nih.gov
Tissue Produrement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Produrement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2499 Std Error: 0.00
Seq primer: -400P from Gibco
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LONGOLL XI NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2073045 3',
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(Dases 1 to 356)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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BQ677668
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 A1475638 tc86d11.x
BM690352 UI-E-CIO-
RS8841 y989d01.x1
BE383336 601298249
BE260495 6011298656
                                                                                       May 17, 2003, 15:56:54 ; Search time 1090.13 Seconds (without alignments) 11900.029 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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                                                BM690352
UI-E-CIO-aah-b-03-0-UI.rl UI-E-CIO Homo sapiens cDNA clone
UI-E-CIO-aah-b-03-0-UI.s', mRNA sequence.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TATTAGCTCCTCAAAGCAAAGCAGGAGAGACAGAAATTTCTGCAGTTGCTTCTTGGTCCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GTCCAAAGCAGACATCAGCCTCTGAACCATCAGCAGTCTTCCTAGTGGCAGTGACTCTCT 240
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Pred. No. 1.6e-62;
1; Mismatches 1; Indels
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                                      /organism="Homo sapiens"
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High quality sequence stop: 351.
Location/Qualifiers
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Best Local Similarity 99.4%;
Matches 354; Conservative
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Hilliatr,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Fax: 319 335 9565
Email: msoares@blue weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M13 Reverse.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IMAGE:40931 5' similar to SP:YK59 YEAST P36159 HYPOTHETICAL 96.8
PROTEIN IN SIS2-MTDI INTERGENIC ; mRNA sequence.
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iive 1; Mismatches 17
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Matches 156; Conservative
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Matches 156; Conservative
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//dev stagge="73 days post natal"
//lab_host="DH10B (ampicillin resistant)"
//note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not
1: Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [A AACTGGAGGAATTTTTTTTTTTTTTT]
AACTGGAAGAATTTTTTTTTTTTTTTT 3'];
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 664)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 61108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1777
High quality sequence stops: 387 Source: IMAGE Consortium, LLNL
This Glone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1777 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGGCAGTGACTCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
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Email: cgapbs-r@mail.nih.gov
Issue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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ilarity 89.1%; Pred. No. 5.6e-20;
Conservative 1; Mismatches 18
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                                                                                                                                                                                                                                                                                             1. .482
/organism="Homo sapiens"
                                                                                                                                                                                                           Insert Length: 1777 Std Error:
Seg primer: MJSRP1
High quality sequence stop: 387.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      /db_xref="GDB:413472"
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                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:40931"
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/db_xref="traxon:050f0".
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 676)

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI76 row: d column: 01
High quality sequence stop: 672.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov Plate: LLCM313 row: a column: 13
High quality sequence stop: 662.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:3503184"
/clone_lib="NIH_MGC_19"
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601298656F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3629028 5',
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/note="Organ: brain, Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGGACGAG(0). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                 338 AGIGGCAGIGACTCTCTTCTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                                                                                                                                                                                 394 ATTCGADATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 453
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 692)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                454 TGTGGTGAGGGCACATTTGGGCAGCTGTGCTCATTACGGAGACCAGGTGGACAGGGTC
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89.1%; Pred. No. 5.2e-20;
ive 1; Mismatches 18
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BE382353
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 698)
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Location/Qualifiers
                                                                                                                     338 AGTGGCAGTGACTCTTCTTTTTTTTTTTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
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                                                             Gaps
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                     CTGGGCACCCTGGCTGCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACGC 512
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Score 145.8; DB 10; Length 692; Pred. No. 5.2e-20;
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                                                             Indels
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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
                                                             18;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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  18.2%;
89.1%;
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Homo sapiens
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/db_xref="taxon:9606"
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/clone="lh="MIH-MGC_41"
/clone="lh="MIH-MGC_41"
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/tab_host="DH10B (phage-resistant)" it issue type="samelanotic"
/lab_host="DH10B (phage-resistant)" it issue line"
/note="organ: skin; Vector: pOTB7; site 1: Xho1; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/Xho1 sites using the following 5; adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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                                                                                                                                                                                                                  BM009099 726 bp mRNA linear EST 30-OCT-2001
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1912 row: o column: 14
High quality sequence stop: 636.
Location/Qualifiers

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1. 726
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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  TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
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Matches 156; Conservative 1; Mismatches 18
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RESULT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 756)

1 (Dases 1 to 756)

1 (Mag. noi.nih.gov/.

1 National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

2 Contact: Robert Strausberg, Ph.D.

2 Email: cgapba-r@mail.nih.gov

7 Issue Procurement: ATC

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: Incytte Genomics, Inc.

DNA Sequencing by: Incytte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM11258 row: k column: 09
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BI257580 756 bp mRNA linear EST 17-JUL-2001
602967138F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5106944 5',
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/tissue_type="cervical carcinoma cell line"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.1e-20;
1; Mismatches 18; Indels 0;
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Location/Qualifiers
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BI257580.1 GI:14813096
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89.1%;
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                                                                        mRNA sequence.
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                                                                                                                                                                                                                                                                                                               /db_xref="taxon:0506"
/clone="IMAGE:3945085"
/clone="IMAGE:3945085"
/clone="IMAGE:3945085"
/clone="IMAGE:3945085"
/clone="IMAGE:3945085"
/cell_line="MGC3"
/lab_host="MHOB (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site_2: EcoR1; CDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGGAGAG(G). Size-selected >500bp for average insert size 1: Nab. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Carlifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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AGENCOURT_8208640 NIH_MGC_102 Homo sapiens CDNA clone IMAGE:6254562
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1 (bases 1 to 874)

NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM802 row: p column: 14
High quality sequence stop: 761.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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89.1%; Pred. No. 5.1e-20;
iive 1; Mismatches 18
                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Unpublished (1999)
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BQ674529
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/clone lib-wink MCCl02"
/tissue type="epidermoid carcinoma, cell line"
/lab host="NIH MGCl02"
/lab host="DH10B (phage-resistant)"
/note="Organ: salivary gland, Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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AGENCOURT 8039759 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6210029
5/, mRNA Sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2370 row: e column: 06
High quality sequence stop: 708.
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NIH-MGC http://mgc.nci.nih.gov/.
National Intsitutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/clone lib="MNH MGC 110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="PH108 (phage-resistant)"
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1; Mismatches 18; Indels
column: 19
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6254562"
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/db_xref="taxon:9606"
                              High quality sequence stop: 6
Location/Qualifiers
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18.2%;

Best Local Similarity 89.1%;

Matches 156; Conservative 1
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Similarity
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                                              Matches 156;
      Query Match
Best Local 9
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/tissue_type="neuroblastoma"
/lab host="NH10B (phage-resistant)"
/lab host="NH10B (phage-resistant)"
/note="Organ: brain; Vector: POTB7; Site 1: XhoI; Site 2: EcoR1; CDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
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Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG519751 884 bp mRNA linear EST 02-APR-2001 602578902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503184 5',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 884)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Colone distribution: M.G.C. clone distribution: M.G.C. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM176 row: d column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                      338 AGTGGCAGTGACTCTTTCTCTTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                              DB 14; Length 876;
                                                                                                                                                                     1 others
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Pred. No. 4.9e-20;
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Location/Qualifiers
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/clone="IMAGE:3503184"
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Tissue Procurement: ATCC
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Best Local Similarity 89.1%;
Matches 156; Conservative 1
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BASE COUNT ORIGIN

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FccR1: cDNA made by oligo-dT priming Directionally
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adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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18.2%; Score 145.8; DB 12; Length
89.1%; Pred. No. 4.9e-20;
vative 1; Mismatches 18; Indels
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Pred. No. 4.9e-20;
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/clone="IMAGE:608996"
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/note="Organ: skin; Vector: poTFF7; Site 1: XhoI; Site_2:
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/gGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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1. (Dases 1 to 915)

2. NIH-MGC http://mgc.nci.nih.gov/.

3. NIH-MGC http://mgc.nci.nih.gov/.

3. NIH-MGC http://mgc.nci.nih.gov/.

4. Ontact: Robert Strausberg, Ph.D.

5. Email: cgapbs-remail.nih.gov

6. Contact: Robert Strausberg, Ph.D.

7 issue Procurement: DcTD/DTP

7 cDNA Library Preparation: Rubin Laboratory

7 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL at:

8 cloud through the I.M.A.G.E. Consortium/LLNL at:

8 high quality sequence stop: 720.

9 Location/Qualifiers
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AGENCOURT_8071095 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089876
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                         533 CTGGGCACCCTGGCTGTGTTTTGTGTCCCACCTGCACGCAGATCACCACACGG 587
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BQ890505
BQ890505.1 GI:22282519
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Search completed: May 17, 2003, 18:18:28 Job time : 1096.13 secs Sequence 379, App Sequence 13, Appl Sequence 296, App

Sequence 583, App Sequence 251, App Sequence 255, App Sequence 267, App Sequence 144, App Sequence 114, App Sequence 112, App Sequence 1166, Ap Sequence 1546, Ap Sequence 1546, Ap Sequence 1546, Ap Sequence 1616, App Sequence 1619, App Sequence 1619, App

Run on:

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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sanatd, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Cene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 1200-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
NUMBER: OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 26664
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10 US-09-764-853-379

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10 US-09-918-995-24438

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ORGANISM: Homo sapiens
FEATURE:
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NAME/KEY: misc_feature

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Sequence 3, Appli
Sequence 30, Appli
Sequence 20, Appl
Sequence 21, App
Sequence 221, App
Sequence 1517, Ap
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1: /cgn2_6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/DEO6 NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
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US-09-988-626-223
US-09-988-626-3
US-09-988-626-3
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OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23: OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation OTHER INFORMATION: signal: 26447-26452

NAME/KEY: variation
LOCATION: (286)..(23879)
OTHER INFORMATION: positions 826 and 23180 is G or C; y at OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at COTHER INFORMATION: is C or T; n at a continuous 22211 and 23879 is A or G.
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                                                                                                                                                                                                            100.0%; Score 800.6; DB 9; Length 26664; 100.0%; Pred. No. 6.4e-234;
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US-09-988-626-28
                                                                                                                                                                                                             Query Match
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APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT APPLICATION NUMBER: 09/564,805
PRIOR PILING DATE: 2000-05-05
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
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OCHER INFORMATION: (13104)

OCHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;

OCHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
OCHER INFORMATION: 13032-13104;

NAME/KEY: misc feature
LOCATION: (13756). (22917)

OCHER INFORMATION: 13: 16278-16416; exon 12: 15283-15378; exon 15: 0THER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15: 0THER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15: 0THER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 17: 0THER INFORMATION: 22172-22310; exon 18: 22879-22917

NAME/KEY: misc feature
LOCATION: (23045). (2642)

OCHER INFORMATION: 25172-22310; exon 18: 22879-22917

NAME/KEY: misc feature
LOCATION: exon 19: 20045-23154; exon 20: 23795-23895; exon 0THER INFORMATION: exon 19: 2045-24432; exon 23: 0THER INFORMATION: 25026-25170; exon 23: 24354-24432; exon 23: 0THER INFORMATION: signal: 26447-26452

OCHER INFORMATION: signal: 26447-26452

OTHER INFORMATION: signal: 26447-26452

OTHER INFORMATION: storions 1914, 5568, 7165, 16431, 1857 and 20486

OTHER INFORMATION: positions 1211 and 23879 is A or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGCCTTTGTGTAAGTCTACTTGAAAGGGTTTCAGGGTTCCATGGATACTTCTTTGCTA 21979
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; Sequence 28, Application US/09988687; Publication No. US20030045704A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc feature
LOCATION: (910)..(13104)
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Orthologous Genes
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Publication No. US20030044959A1
GENERAL INFORMATION:
APPLICANT: Tavitigian, Sean V.
APPLICANT: Tavitigian, Sean V.
APPLICANT: Tavitigian, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
ITLE OF INVENTION: Chromosome 17p-Linked Prost.
ITLE OF INVENTION: Gene and a Paralog and Orti;
FILE REPERENCE: 2318-258
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR APPLICATION NUMBER: 09/64,805
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE PLENCY DE NOS: 240
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NAME/KEY: CDS
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LENGTH: 2481
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APPLICANT: Tavtidian, Sean V.
APPLICANT: Tavtidian, Sean V.
APPLICANT: Tavtidian, Sean V.
APPLICANT: Tavtidian, Jacques
APPLICANT: Simard, Jacques
Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT PILING DATE: 2000-05-05
RRIOR FILING DATE: 2000-05-05
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
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  Score 145.8; DB 9; Length
Pred. No. 6.8e-34;
1; Mismatches 18; Indels
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Pred. No. 6.8e-34;
1; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09988687; Publication No. US20030045704A1; GENERAL INFORMATION:
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89.1%;
Query Match
Best Local Similarity 89.1%;
Matches 156; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
LENGTH: 2481
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Matches 156; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , LOCATION: (1)..(2478)
US-09-988-687-1
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US-09-988-626-225
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; LOCATION: (1)
US-09-988-687-225
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SEQ ID NO 223
LENGTH: 2908
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US-09-988-626-223
                                                                              Query Match
Best Local
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APPLICANT: Tavitigian, Sean V.
APPLICANT: Tavitigian, Sean V.
APPLICANT: Tavitigian, Jacoba H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2000-05-05
PRIOR PLILING DATE: 2000-05-05
PRIOR PLILING DATE: 1998-11-06
PRIOR PLILING DATE: 1998-11-06
PRIOR PLILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 225
LENGTH: 2892
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Jacque H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Jacques
APPLICANT: Rommens, Jacques
APPLICANT: Rommens, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PRECEIN VET: 2.0
SOFTWARE: PERCEIN VET: 2.0
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Pred. No. 7.5e-34;
1; Mismatches 18; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.1%;
Matches 156; Conservative
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ORGANISM: Gorilla gorilla
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Gorilla gorilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-988-626-225
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APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sand H.F.
APPLICANT: Simard, Jacques
Simard, Jacques
Taridicant: Rowmens, Johanna M.
APPLICANT: Rowmens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 218-28
CURRENT APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR APPLICATION NUMBER: 09/11-05
NUMBER OF SEQ ID NOS: 240
SOCTHWARE: PatentIn Ver: 2.0
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Best Local Similarity 89.1%; Pred. No. 7.5e-34;
Matches 156; Conservative 1; Mismatches 18;
                                                                                           DB 9;
                                                                                        Score 145.8; DB 9
Pred. No. 7.5e-34;
                                                                                                                                                     1; Mismatches
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; Sequence 223, Application US/09988626
; Publication No. US20030044959A1
; GENERAL INFORMATION:
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US-09-988-687-223
; Sequence 223, Application US/09988687
                                                                                        18.2%;
ilarity 89.1%;
Conservative
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ORGANISM: Pan troglodytes
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Matches 156; Conserv
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Similarity
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Best Local Simi:
Matches 156;
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                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Johanna M.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2118-258
CURRENT APPLICATION NUMBER: US/09/988,687
FILE REPLIANT FILING DATE: 2001-01-20
FRIOR FILING DATE: 1999-11-06
FRIOR FILING DATE: 1999-11-06
FRIOR FILING DATE: 1999-11-05
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Sequence 3, Application US/0998626

Publication No US20030044959A1

GENERAL INPORMATION:

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Romens, Johanna M.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,626

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PatentIN Ver. 2.0
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Pred. No. 7.5e-34;
1; Mismatches 18;
Publication No. US20030045704A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.1%;
Matches 156; Conservative
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ORGANISM: Homo sapiens
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US-09-988-687-223
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LENGTH: 2958
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APPLICANT: Tavidian, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
FILE REFERENCE: 2001-11-20
PRIOR FILING DATE: 2001-11-06
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARR: PACENTIN VET. 2.00
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                                                                                                                                                                                                   Length 2958;
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51)...(2531)
; OTHER INDEWATION: coding sequence as in SEQ ID NO:1
US-09-988-626-3
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LOCATION: (51)...(2531)
OTHER INFORMATION: coding sequence as in SEQ ID NO:1
                                                                                                                                                                                                Score 145.8; DB 9;
Pred. No. 7.6e-34;
1; Mismatches 18;
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ilarity 89.1%;
Conservative 1
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SEQ ID NO 20
LENGTH: 139
TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 2470
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                                               Sequence 20, Application US/09988626

Sequence 20, Application US/09988626

Bublication No. US20030044959A1

GENERAL INFORMATION:

APPLICANT: Tavitigina.

APPLICANT: Tavitigina.

APPLICANT: Simard, Jacques

APPLICANT: Rowmens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Cance and a Paralog

TITLE OF INVENTION: Cance and a Paralog

CURRENT APPLICATION NUMBER: US/09/988,626

CURRENT FILING DATE: 2000-05-05

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 20

LENGTH: 139

TUBLE OF TAVITION NUMBER: US OF TAVITION NUMBER: US
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Sequence 20, Application US/0988687

Publication No. US20030045704A1

GENERAL INFORMATION:

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Simard, Jacques

APPLICANT: Simard, Jordnam M.

TITLE OF INVENTION: Chromosome 17p-linked Prostate Cancer Susceptibility

TITLE OF INVENTION NUMBER: 109/564, 805

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR APPLICATION NUMBER: 09/434, 382

PRIOR FILING DATE: 1999-11-06

PRIOR SEQ ID NOS: 240

NUMBER OF SEQ ID NOS: 220

NUMBER OF SEQ ID NOS: 220
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Pred. No. 1.8e-32;
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Best Local Similarity 99.3%;
Matches 138; Conservative
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| LOCATION: (1)..(139)

| OTHER INFORMATION: exon 17

US-09-988-626-20
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US-UN-988-beloaded

US-UN-988-beloaded

US-UN-988-beloaded

Publication No. US20030044959A1

GENERAL INFORMATION:

APPLICANT: Tavidgian, Sean V.

APPLICANT: Tavidgian, Sand V.

APPLICANT: Tavidgian, Sand V.

APPLICANT: Romens. Johanna

APPLICANT: Romens. Johanna

APPLICANT: Myriad Genetics Inc.

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,626

CURRENT FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR PLING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

NUMBER OF SEQ ID NOS: 240

NUMBER OF SEQ ID NOS: 240

NUMBER OF SEQ ID NOS: 240
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                                                                                                                                                       Length 139;
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Pred. No. 1.6e-20;
0; Mismatches 43;
                                                                                                                                                         DB 9;
                                                                                                                                                       Score 138.6; DB 9,
Pred. No. 1.8e-32;
1; Mismatches 0;
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Best Local Similarity 99.3%;
Matches 138; Conservative
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FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(139)
CTHER INFORMATION: exon 17
US-09-988-687-20
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Matches 128; Conservative
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US-09-988-626-221
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                                                                                                                                                                                                                              APPLICANT: Simard, Jacque n.s.
APPLICANT: Simard, Jacque n.s.
APPLICANT: Somens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 221
LENGTH: 2470
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1571 GCAGCCTCACGGCTGTTTGTGTCCCCACCTGCACGCCGACCACCACGG 1621
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CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 1517
LENGTH: 1152
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                                                                                                                      Sequence 221, Application US/09988687
Publication No. US20030045704A1
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
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US-10-092-154-1517
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US-09-988-687-221
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Best Local Similarity
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Best Local Similarity
Matches 128; Conserv
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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      SOFTWARE: Pater
SEQ ID NO 28
LENGTH: 26664
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Sequence 225, App
Sequence 223, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 25, Appli
Sequence 261, Appli
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Sequence 261, Appli
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Sequence 1, Appli
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                                                                                                                                                 May 17, 2003, 15:56:54 ; Search time 45.0714 Seconds (without alignments) 5450.193 Million cell updates/sec
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Sequence 1, Ap
Sequence 10, P
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Sequence 17,
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                  GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-564-805-223
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Listing first 45 summaries
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c 29 32.8 4.1 8967 1 US-08-366-851A-1 Sequence 1, Appli Sequence 3, Appli 23.8 4.1 9009 1 US-08-251-9704-3 Sequence 3, Appli C 31 32.8 4.1 9009 1 US-08-251-937A-3 Sequence 1, Appli C 34 32.8 4.1 9009 1 US-08-474-501. Sequence 1, Appli C 35 32.8 4.1 9009 2 US-08-7474-501. Sequence 1, Appli C 35 32.8 4.1 9009 2 US-08-707A-1 Sequence 1, Appli C 35 32.8 4.1 9009 4 US-09-037-601-1 Sequence 1, Appli C 37 32.8 4.1 9009 4 US-09-52-656-1 Sequence 1, Appli C 37 32.8 4.1 9009 5 PCT-US93-0325-3 Sequence 1, Appli C 38 32.8 4.1 9009 5 PCT-US91-03275-3 Sequence 1, Appli C 38 32.8 4.1 9009 5 PCT-US91-03275-3 Sequence 1, Appli C 38 32.8 4.1 9009 5 PCT-US91-03275-3 Sequence 1, Appli C 38 32.8 4.1 9009 5 PCT-US91-03275-3 Sequence 2, Appli C 32.8 4.0 630 6 US-08-952-736A-4 Sequence 1, Appli C 32.3 4.0 630 6 US-08-952-736A-4 Sequence 2, Appli C 32.2 4.0 1356 4 US-08-952-736A-1 Sequence 2, Appli C 32.2 4.0 1356 4 US-09-149-476-281 Sequence 131, Appli C 45 31.8 4.0 1008 4 US-09-149-476-281 Sequence 130, Appli C 45 31.8 4.0 1008 4 US-09-149-476-281 Sequence 130, Appli C 45 31.8 4.0 1008 4 US-08-235-836C-130
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ALIGNMENTS

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JOHERANI TAVIDATION SCAIN V.

APPLICANT: Tavidjan, Scan V.
APPLICANT: Tavidjan, Scan V.
APPLICANT: Tavidjan, Scan V.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Cromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Cromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 05 60/107,468
PRIOR APPLICATION NUMBER: 09434,382
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
  Chromosome 17p-Linked Prostate Cancer Susceptibility
Gene and a Paralog and Orthologous Genes
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18.2%; Score 145.8; DB 4;
Best Local Similarity 89.1%; Pred. No. 3.8e-34;
Matches 156; Conservative 1; Mismatches 18;
TITLE OF INVENTION: Chromosome 17p-Linked P TITLE OF INVENTION: Gene and a Paralog and FILE OF INVENTION: Gene and a Paralog and FILE OF INVENTION: Gene and a Paralog and CHROMER APPLICATION NUMBER: US/09/564,805 PRIOR APPLICATION NUMBER: US 60/107,468 PRIOR PILING DATE: 1998-11-06 PRIOR APPLICATION NUMBER: 09/434,382 PRIOR FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 240 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 225, Application US/09564805
; Patent No. 6333403
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                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: (1)..(2478)
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; LOCATION: (1)..(2478)
US-09-564-805-225
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Best Local Simil
Matches 156; C
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                                              100.0%; Score 800.6; DB 4; Length 26664; 100.0%; Pred. No. 7.6e-232;
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US-09-564-805-1
; Squence 1, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION;
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Romens, Johanna N.
; APPLICANT: Romens, Johanna M.
; APPLICANT: Romens, Johanna M.
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                                                                   Best Local Similarity 100.
Matches 801; Conservative
        US-09-564-805-28
                                                Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Taviguan H.F.
APPLICANT: Simand, Joqques
APPLICANT: Simand, Joqques
APPLICANT: Simand, Joqques
APPLICANT: Myriad Genetics, Inc.
ITILE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 099411-05
PRIOR APPLICATION NUMBER: 099411-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 223
LENGTH: 2908
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APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
  1486 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1545
                                                                        1486 ATTCGAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1545
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Patent No. 6333403
PATENTAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
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Patent No. 6333403
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match .18.2%
Best Local Similarity 89.1%
Matches 156; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-564-805-223
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JAPPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Sinard, Jacques
APPLICANT: Sinard, Jacques
APPLICANT: Sinard, Jacques
TITLE OF INVENTION: Gene and A Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and A Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and A Paralog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 4.2e-34;
1; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEX: misc_feature
LOCATION: (51)...(2531)
COTHER INFRAMION: coding sequence as in SEQ ID NO:1
US-09-564-805-3
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PRIOR APPLICATION NUMBER: US 60/107,4 PRIOR FILING DATE: 1998-11-06 PRIOR APPLICATION NUMBER: 09/434,382 PRIOR FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 240 SOFTWARE: PALENTIN Ver. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 20, Application US/09564805; Patent No. 6333403
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Matches 156; Conservative 1
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99.3%;
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LOCATION: (1)...(139)
OTHER INFORMATION: exon 17
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Matches 138; Conservative
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tang, David H.F.
APPLICANT: Sinard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: 108/09/564,805
CURRENT FILING DATE: 2000-05-05
FRIOR APPLICATION NUMBER: 05/0107,468
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1999-11-05
FRIOR APPLICATION NUMBER: 09/434,382
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TTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTTTTGTGTCTCCACCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 GCAGTGACTCTTCCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGACTGTG 401
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6e-21;
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                                                                                                                                                                                                                                             Sequence 221, Application US/09564805
Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                          121 GCACGCAGATCACCACG 139
                                                                          GCACGCAGATCACCACACG 511
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Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .. (2466)
                                                                                                                                                                                                                                                                    Patent No. 6333403
GENERAL INFORMATION:
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SEQ ID NO 221
LENGTH: 2470
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LOCATION: (1)
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US-09-564-805-221
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US-09-564-805-221
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590 TICCICCGCTICCAAACTIGCCCAGAGCTTITGTTACTCATCTCTGGCTAGGAAATGGTT 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 7218;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.0%; Score 39.8; DB 1;
ilarity 1.3%; Pred. No. 0.087;
Conservative 214; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence I, Application US/09376728

Batent No. 6372961

GENERAL INFORMATION:
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Shen, Bo
TITLE OF INVENTION: Hemoglobin Genes and Their Use
FILE REPERENCE: 0873
                                                                                                                                                                                                                                                                                                                             TELEFRENCE (703) 683-4109

TELEFAX: (703) 683-4109
                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                    EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1426 YYYYYYYYGTACCA 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-376-728-1/c
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APPLICANT: Su, Xin-zhaun
APPLICANT: wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM PALCIPARUM BRYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 TCAGGGTTCCAŢGGAŢACTTCTŢŢGCTATAAAGAGGATGACACATGTAAAAŢCACCTTTA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 ATAAACTTTTTTTTTTTTTTTGATGCCCAGCCTTTGTGTAAGTCTACTTGAAAGGGTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WASSER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 2436-20007.00
CURRENT APPLICATION UNMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36.6; DB 2; Length 19124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
                                                                                                                                                                                                                                                                                        ADDRESSEE: Knobbe Martens Olson & Bear STRET: 620 Newport Center Drive 16th Floor STRET: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTONERY/AGENT INFORMATION:
NAME: Israelsen, Ned 9,655
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
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...aeR: US/08/487,826B
10-SEP-1993
10-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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   Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 78; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6294328
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-487-826B-13
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US-09-103-840A-2
                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS.AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-108-14
RIOR FILING DATE: 1997-108-14
RIOR FILING DATE: 1997-108-14
RUMBER: OF SEQ ID NOS: 5674
SEQ ID NO 1951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCC 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39.4; DB 4; I
Pred. No. 0.034;
0; Mismatches 76;
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Pred. No. 0.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                          CURRENT FILING DATE: 1999-08-17
EARLIER APPLICATION NUMBER: US 60/097,242
EARLIER FILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 840
CURRENT APPLICATION NUMBER: US/09/376,728
CURRENT FILING DATE: 1999-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1951, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA CORGANISM: Staphylococcus epidermidis US-09-134-001C-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence 13, Application US/084878268 sequence 13, Application US/084878268 sequence 18. Sp3827 sequence 18. Application: APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.9%;
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Best Local Similarity 69.4%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 52.8
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTTTTTGAT 118
                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (51)...(623)
US-09-376-728-1
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                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367
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                                                                                                                                                  OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 435375 GGCTTGTCCCACACGGCGTCGCCGGGGTCCGCCGCACCGCCAGGTCCTGCAACCGGCG 435434
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                                                                                                                                                                                                                                                                                                                                                     419 CAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 CTTCTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGACTGTGGGGGGCACRTTTGGG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FABER, Owen R.
APPLICANT: FARSER, Claire M.
APPLICANT: FARSER, Claire M.
APPLICANT: VERNER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2000/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                               Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 4411529;
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                                                                                                                                                                                                                                                          Score 36.6; DB 4;
Pred. No. 25;
1; Mismatches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                 TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.9%;
Matches 84; Conservative 1
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Matches 84; Conservative
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
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                                                               LENGTH: 4403765
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US-09-103-840A-1
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US-09-103-840A-1
                                        SEQ ID NO 2
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Sequence 261, Application US/09461697 Patent No. 6277974

US-09-461-697-261/c

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APPLICANT: COGRAT NEUROSCIENCE, Inc.
APPLICANT: Donald C.
APPLICANT: Darney, Shawn
APPLICANT: Parrier, Shawn
APPLICANT: Puranem, Kasturi
APPLICANT: Neurance C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOUTHWARE: PASTESEQ for Windows Version 4.0
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TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER FILING NUMBER: 60/040,336
EARLIER FILING NUMBER: 60/040,336
EARLIER FILING NUMBER: 60/040,163
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Pred. No. (
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EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
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Best Local Similarity 51.9%;
Matches 81; Conservative
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CRGANISM: Homo sapiens
US-09-461-697-261
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US-09-149-476-255/c
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LENGTH: 1182
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REFLING DATE: 1997-08-22
RAPPLICATION NUMBER: 60/056,894
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RETLING DATE: 1997-08-22
RETLING DATE: 1997-08-22
RETLING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056, 845
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 892
R TILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/057, 761
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/047, 595
R APPLICATION NUMBER: 60/047, 595
R APPLICATION NUMBER: 60/047, 595
R APPLICATION NUMBER: 60/047, 599
R FILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/047,614
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043,578
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,576
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/047,501
R FILING DATE: 1997-05-23 R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,590
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,594
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,872
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,882
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,879
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,880 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,585 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 APPLICATION NUMBER: 60/056,637 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,588 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,670 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,632 FILING DATE: 1997-08-22 BARLIER PARLIER PARLIE

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ER APPLICATION NUMBER: 60/056,909
ER FILING DATE: 1997-08-22
ER PELING DATE: 1997-08-22
ER PLING DATE: 1997-08-22
ER PELING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,908
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,864
ER FILING DATE: 1997-08-05
ER PLING DATE: 1997-08-05
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. 0 99 ITITITITITITITICALGCCCAGCCTTIGIGTAAGTCTACTTGAAAGGGTTTCAGGG 158 Query Match
4.5%; Score 36; DB 4; Length 2664;
Best Local Similarity 51.9%; Pred. No. 0.7;
Matches 81; Conservative 0; Mismatches 75; Indels

2514 TITITITITITITITITATACCACATCAATITGAAATITACAGGAACCAAGAITCAAG 2455 159 TTCCATGGATACTTCTTTGCTATAAAGAGGATGACACATGTAAAATCACCTTTATGGTTA 218 තු

219 AATTAATTGGCTTTTATATTAGCTCCTCAAAGCAAA 254

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Search completed: May 17, 2003, 17:27:33 Job time: 2436.07 secs

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AU149928 AU149928
AU448489 AU149489
AA862956 G998607.s
AI831155 wj81607.x
                                  A1089646 qb16g07.x

AW11765 xx076f03.x

AA766184 cal12f09.8

A1033108 cw98g08.8

AA23338 zx05h05.s

B003038 UI-H-DT0-AA66504 no47g05.s

AA883412 nn42b10.8

A114263 qa46h05.s

A11527786 qu98d07.x

AN592223 hf41a01.x
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A1803400 cc42£03.x
AA534478 nf76£10.s
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        BO181829 UI-H-EU0-
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AW248468 2820640.3
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BI870047 603393914
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BM353522 ig56c05.x
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AA134386 zo24d10.s
BQ549604 ik88h10.x
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AI804749 tu42d02.x
BF477438 nac60h05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1032)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation
CDNA Library Preparation
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12140 row: n column: 03
High quality sequence stop: 720.
Location/Qualifiers
1. 1032
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BM353522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
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COMMENT
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AW407520 UI-HF-BM0
AA811170 0b42c03.s
AI500718 tn94b10.x
AW592601 hf45a09.x
AW510825 hd40b11.x
                                                          May 17, 2003, 15:56:54 ; Search time 681.842 Seconds (without alignments) 11900.029 Million cell updates/sec
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                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993
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Matches 305; Conserv
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AUTHORS
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              /db_xref="taxon:9606"
/clone="IMAGE:5502530"
/clone lib="NIH MGC 67"
/tissue_type="retinoblastoma"
/lab.host="PHIB (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Technologies."
Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW407520 345 bp mRNA linear EST 16-FEB-2000 UI-HF-BM0-adl-b-07-0-UI.rl NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3061957 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
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                                                                                                                                                                                                                          93.6%; Score 469; DB 13; Length 1032; 97.6%; Pred. No. 2.8e-131; ive 0; Mismatches 5; Indels 7
                                                                                                                                                                          3 others
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organism="Homo sapiens"
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AW407520.1 GI:6926577
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234 c
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/note="Vector: pT/T3-Pac, Site_1: Not1; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (2.5-3.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 396)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Array by M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: Seq primer: MI3 Forward.
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                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="InAGE:306195"
/clone=lib="NIH MGC_38"
/tissue_type="lymph"
/cell_type="lymph"
/cell_line="MGC85"
/lab_nost="DH10B_(LTI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 303.2; DB 10;
Pred. No. 3.7e-81;
0; Mismatches 3;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                              Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 372) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                Tumor Gene Index
Unpublished (1997)
                                Homo sapiens
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0
                                                                                        Sequencing Center information can be
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                  Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Mashington University Genome Seq

Clone distribution: NCI-CGAP clone distribution inf

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrpy/image/himge.html

Insert Length: 885 Std Brror: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 396;
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Best Local Similarity 100.0%; Pred. No. 4.7e-81;
Matches 303; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                    /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:1334020"
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/lab_host="DH108"
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AISO0718 372 bp mRNA linear EST 14-APR-1999 tn994b10.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMACE:2177179 3', mRNA sequence.
AISO0718

AI500718.1 GI:4392700

LOCUS

ACCESSION.

VERSION

A1500718/c

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Parearation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrpy/mage/image.html
Insert Length: 737 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
/note="Organ: uterus, Vector: pCMV-SPORT6, Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 GGTATGGAGCTGTGCCGAGGCTTGGGGTCCCACATAAGCACTAGTCTATAGATGCCTCTT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:2177179"
/clone=lib="NCI_CGAP_Ut2"
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adenocarcinoma, 3 pooled tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTAATCCAGCAAAATGATTCCCTGCACAGAGACAAGCAGAGGTAACAGGATCAGTG
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hf45a09.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2934808 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 302.6; DB 9;
Pred. No. 6e-81;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 t
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                             Seq primer: -40UP from Gibco
High quality sequence stop: 342.
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ilarity 98.7%;
Conservative C
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AWS92601/c
LOCUS
DEFINITION
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/db xref="taxon:9606"
/clone="INAGE:291965"
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/lab host=="Boares_NFL_T_GBC_S1"
/lab host=="Boares_NFL_T_SIGE_I: Not I; Site_2: Eco RI;
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Bqual amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatina Bonaldo. "
126 g 137 t
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                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 499)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco High quality sequence stop: 470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGCGCCCTTTC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 300
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                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
:MAGE:2911965 3', mRNA sequence.
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                       AW510825
AW510825.1 GI:7148903
                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
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Best Local 9
                                                                KEYWORDS
SOURCE
ORGANISM
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AW572950/c
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ORIGIN
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TITLE
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                     ACCESSION
VERSION
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                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 47)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
High quality sequence stop: 451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAGAAAAGCAGAGTAACAGGATCAGTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .478
/organism="Homo sapiens"
/organism="taxon:9666"
/clone="IMAGE:2934808"
/clone lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.2%; Score 301.4; DB 1(99.7%; Pred. No. 1.6e-80; iive 0; Mismatches 1
                       GI:7279786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 302; Conservative
                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                       AWS92601.1
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                                                                       human.
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Glone="INGEC:932818"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="Bluble"
/lab_host="Bluble"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento
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                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 531)
                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infl@image.llnl.gov) for further information.
Seg primer: -40UP from Gibco
                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.2%; Score 301.4; DB 10; Length 531; larity 99.7%; Pred. No. 1.8e-80; Conservative 0; Mismatches 1; Indels 0;
hf17h05.x1 Soares_NPL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2932185 3', mRNĀ sequence.
                                                                                                                                                                                                                                                                                                                                        Seq primer: -40UP from Gibou
High quality sequence stop: 459.
Location/Qualifiers
1. 531
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 g
                                                         AW572950.1 GI:7237683
                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
                                                                                                                    Homo sapiens
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                                                                                                                                                                                        AUTHORS
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RESULT 8 BQ181829/c

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/db xref="taxon:9606"
/clone="IMAGE: 585425"
/dev_stage="Adult"
/lab host="DH108 (Life Technologies)"
/lab host="DH108 (Life Technologies)"
/note="Organ: Knee; Vector: pT773-pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
NCI_CGAP_Carl is a cDNA library containing the following tissue (s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the manner of the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the
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                                             EST 30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POUYA=Yes.
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 692) NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
692 bp mRNA linear EST 30-APR-1
UI-H-EU0-azv-m-08-0-UI.s1 NCI_CGAP_Carl Homo sapiens cDNA clone
IMAGE: 5854255 3', mRNA sequence.
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Pred. No. 2.1e-80;
0; Mismatches 1; Indels 0;
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TAG_LIB=UI-H-EU0
TAG_TISSUE=osteoarthritic cartilage
TAG_SEQ=TGATCACGCT"
TAG_SEQ=TGATCACGCT"
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99.7%;
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Unpublished (1997)
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Best Local Similarity 99.7
Matches 302, Conservative
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DB 14; Length 712; 1; Indels

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Consolis capabs-remail.nih.gov

Final: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consoctium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found throughthe I.M.A.G.E. Consortium/Lubin at:

www-bio.lln.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center.

Trimming: cross match from University of Washingtion Genome Center.

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washingtion Genome Center:

http://www.genome.washington.edu Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues

at the beginning of the sequence, this CDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW248468 394 bp mRNA linear EST 07-JAN-2000
282640.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820640 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 394)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2820640.5prime
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                           319 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 260
                                                                                                                                                                                                                                   259 AGGACTGGCTGGCACAGCCGCGGGCCAGGAGGCTGCCACACGGAAGCAGAGAGA 200
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/clone_lib="NIH_MGC_7"
fissue type="small_cell_carcinoma"
/cell_line="MGC3"
Score 301.4; DB 14
Pred. No. 2.2e-80;
0; Mismatches 1;
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High quality sequence stop: 213.
Location/Qualifiers
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  60.2%;
  Query Match
Best Local Similarity 99.77
Matches 302; Conservative
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TITLE
JOURNAL
COMMENT
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/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/note="Organ: Lung; Vector: pr713-pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
UI-CF-ENI is a normalized—CDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dr primer containing a Not I shte. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligomiclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (d7)18 tail. The sequence tag for this library is CTGCTCAGGT.
TAG_LIBEUI-CF-ENI
TAG_TISSUB=Human Lung Epithelial Cell Lines untreated LPS for the LDES 24hm.
                                                                                                                                                                                                                                                                                   UI-CF-EN1-aef-c-19-0-UI.sl UI-CF-EN1 Homo sapiens cDNA clone
BM977567
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa
2024 University of Iowa
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Email: paul-mccray@uiowa.edu
CINS Library preparation: Dr. M. J. Welsh, University of Iowa
CINS Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CIONE Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens .

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 712)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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/clone="UJ-CF-EN1-aef-c-19-0-UI"
/clone_lib="UI-CF-EN1"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
     241 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 300
                                      79 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 20
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_211 c 176 q
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ORIGIN
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FEATURES

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE

19

g ò AUTHORS TITLE

REFERENCE

MEDLINE COMMENT

JOURNAL

임 ò 셤 ò g ઠ 硆 ò g ò 엄

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/organism="Homo sapiens"
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0
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTPB; Site 1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500Dp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
103 c 97 g 114 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LiNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 463.
Location/Qualifiers
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                                                                                                                                                                                                                        59.8%; Score 299.8; DB 10; Length 394; 99.3%; Pred. No. 4.4e-80; ive 0; Mismatches 2; Indels 0;
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/clone="IMAGE:1696476"
/clone_lib="Soares_pregnant_uterus_NbHPU"
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National Cancer Institute, Cancer Genome Anatomy
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/dev_stage="adult"
/lab_host="DH10B"
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AI089646.1 GI:3428705
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Unpublished (1997)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gloco
High quality sequence stop: 239.
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180
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National Cancer Institute, Cancer Genome Anatomy Project
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Unpublished (1997)
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AW511765.1
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410 bp mRNA linear EST 28-AUG-1998 clone IMAGE:1654910 3', mRNA sequence. AI033108
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Vakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 410)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: Gagabs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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              /organism="Homo sapiens"
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Const Library Arrayed by: Greeg Lennon, Ph.D.

CDNA Library Arrayed by: Greeg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Mow-bio.llnl.gov/bbrp/limage.html

Insert Length: 1277 Std.Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stope: 288

Location/Qualifiers
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          /clone_lib="NCI_CGAP_Kid8"
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/tissue_type="renal_cell tumor"
/lab_host="BH10B"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_l: Sall;
Site_2: NOtel; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.2 kb. Life Technologies catalog #:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 318)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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1 (bases 1 to 374)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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/scs="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 298.2; DB 9; Length 410;
Pred. No. 1.4e-79;
0; Mismatches 3; Indels 0;
Insert Length: 773 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 368.
Location/Qualifiers
                                                                l. .410
organism="Homo sapiens"
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Best Local Similarity 99.0%;
Matches 300; Conservative (
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Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wastson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 3011 Std Brror: 0.00

Seq primer: -41nnl % Tel from Amersham.

Location/Qualifiers
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/db_xref="tanon:9606"
/clone="InhAGE:650649"
/clone=lib="Stratagene NT2 neuronal precursor 937230"
/tissue_type="neuroepithenial cells"
/dev_stage="Ntext=2 neuroepithenial cells"
/lab_host="SOLR (kanamycin resistant)"
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
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OTHER INFORMATION: 1856
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LENGTH: 26664
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Sequence 4, Appli
Sequence 2320, Ap
Sequence 2145, Ap
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Sequence 206, App
Sequence 107, App
                                                                            May 17, 2003, 17:27:39 ; Search time 63.5169 Seconds (without alignments) 10174.595 Million cell updates/sec
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Sequence 3, Appli
Sequence 223, App
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/ cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-988-626-3
US-09-988-687-3
US-09-988-687-223
US-09-988-626-225
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US-09-809-391-107
US-09-917-800A-1269
US-09-960-352-8591
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US-09-880-107-2145
US-09-887-576-655
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Maximum Match 100%
Listing first 45 summaries
                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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ALIGNMENTS

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US-09-988-626-28
Sequence 28, Application US/0998626
Publication No. US20030044959A1
GENERAL INCORMATION:
APPLICANT: Tarticidan, Sean V.
APPLICANT: Tarticidan, Sean V.
APPLICANT: Tarticidan, Sean V.
APPLICANT: Treng David H.F.
APPLICANT: Rommend: Johnan M.
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APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sanard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT PILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/664,805
PRIOR APPLICATION NUMBER: US/664,805
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
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OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon 21: 0THER INFORMATION: 25026-22170; exon 24: 25812-26036; polyadenylation OTHER INFORMATION: signal: 26447-26452

NAME/KEY: variation
LOCATION: (826)..(23879)
OTHER INFORMATION: s at positions 826 and 23180 is G or C; y at OTHER INFORMATION: positions 1914, 5568, 7165; 16431, 1857 and 20486; OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at US-09-988-626-28
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100.0%; Pred. No. 1.7e-160;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.7e-160;
tive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 26664
TYPE: DNA
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Best Local Similarity 100.0
Matches 501; Conservative
                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION UNMERR: US/09/988,687
CURRENT APPLICATION NUMBER: 09564,805
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1999-11-05
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Publication No. US20030044959A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Simard Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE CONTRENT APPLICATION NUMBER: US/09/988,626
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Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 303; Conservative 0; Mismatches 0;
     Tavtigian, Sean V. Teng, David H.F.
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION: exon
NAME/KEY: polyA_signal
LOCATION: (636)..(641)
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LOCATION: (1)..(228)
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LENGTH: 655
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US-09-988-626-3
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APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sacques
APPLICANT: Tavtiglan, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 218-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT PILING DATE: 2001-01-20
PRIOR APPLICATION NUMBER: US/06.05
PRIOR APPLICATION NUMBER: US/06.05
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 27
LENGTH: 655
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Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 303; Conservative 0; Mismatches 0; Indels
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Publication No. US20030045704A1
GENERAL INFORMATION:
                                                                                                                                                     Sequence 27, Application US/09988626
Publication No. US20030044959A1
GENERAL INFORMATION:
Db 26644 ATTCGCCAAGTCTTTTTGACA 26664
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NAME/KEY: misc_feature
LOCATION: (1)...(228)
OTHER INFORMATION: exon 24
NAME/KEY: polyA signal
LOCATION: (636)...(641)
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ORGANISM: Homo sapiens
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US-09-988-687-27
                                                                                                                                US-09-988-626-27
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, David H.F.
APPLICANT: Tavtigian, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
ITILE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 218-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT APPLICATION NUMBER: US/054,805
FRIOR APPLICATION NUMBER: US/054,805
FRIOR FILING DATE: 1998-11-06
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1998-11-06
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1999-11-05
SOFTWARE: ParentIn Ver. 2.0
SOFTWARE: ParentIn Ver. 2.0
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                                                                                                                                                                                                             Length 2958;
                                                                                                                                                                                                                                                            Indels
                            ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (51)...(2531)
OTHER INFORMATION: coding sequence as in SEQ ID NO:1US-09-988-687-3
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                                                                                                                                                                                                        60.5%; Score 303; DB 9; I
100.0%; Pred. No. 4.3e-93;
live 0; Mismatches 0;
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Publication No. US20030044959A1
GENERAL INFORMATION:
                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 303; Conservative
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Best Local Similarity 98.7
Matches 299; Conservative
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NAME/KEY: CDS

LOCATION: (1)..(2478)

US-09-988-626-223
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GENERAL INFUGUATION:
GENERAL INFUGUATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Jacques
APPLICANT: Tavtigian, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2118-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
SPIOR FILING DATE: 1999-11-05
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2958
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100.0%; Pred. No. 4.3e-93;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                            LOCATION: (51)...(2531)
CTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-988-626-3
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 2000-05-05
PRIOR PILING DATE: 1098-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PATENT Ver. 2.0
LENGTH: 2958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 303; Conservative
                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: (51)..(2531)
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; LOCATION: (1)..(2478)
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US-09-988-626-225
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Sequence 223, Application No. US20030045704A1

GENERAL INFORMATION:

APPLICANT: Tavitisian. Sean V.

APPLICANT: Tavitisian. Volanna M.

APPLICANT: Rommens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Ghromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

CURRENT APPLICATION NUMBER: US/09/988,687

CURRENT FILING DATE: 2000-05-05

PRIOR FILING DATE: 12998-11-06

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 223

LENGTH: 2908
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; LOCATION: (1)..(2478)
US-09-988-687-223
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US-09-988-687-223
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PAPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sana H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
Tapticant: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT FILIAN DATE: 2000-05-05
PRIOR PILING DATE: 2000-05-05
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
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2786 CTCTAATCCAGCAAAGTGATTCCCCTGCACACAGAGACAAGCAGAGTAACAGGATCAGTG
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Pred. No. 1.7e-76;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 225, Application US/09988626; Publication No. US20030044959A1; GENERAL INFORMATION:
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93.4%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 225
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Best Local Similarity 93.4
Matches 283; Conservative
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236 CAGTGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01.30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 15427
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.7%; Score 33.6; DB 10; 47.2%; Pred. No. 0.44;
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PRIOR PELLING DATE: 2001-03-23
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-36
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MAP TO AC009230.2
OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN BT474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 102; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-864-761-15427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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APPLICANT: Penn, Sharron G.
APPLICANT: Ranzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENERESSION ANALYSIS BY MICROARRAY
                                                                                          APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Jacques
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Jacques
APPLICANT: Rommens, Jacques
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2770 CTCTAATCCAGGAAAGTGATTCCCTGCACACAGAGACAAGCAGAGTAACAGGATCACTG 2829
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Pred. No. 1.7e-76;
0; Mismatches 4;
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            ; Sequence 225, Application US/09988687
; Publication No. US20030045704A1
; GENERAL INFORMATION:
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ilarity 93.4%;
Conservative
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Matches 283; Conserv
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, LOCATION: (1)
US-09-988-687-225
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LENGTH: 2892
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Length 480;

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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown, D.
Chang, H.
Zhu, T.
Han, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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US-09-880-107-2145
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                                                                                                                                                                                       APPLICANT: Hauge, Brian M.
APPLICANT: Hauge, Jeremy D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR PRILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.4%; Score 32.2; DB 9; Length 513509; Best Local Similarity 66.7%; Pred. No. 69; Matches 46; Conservative 0; Mismatches 23; Indels 0;
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| Patent No. US20020146721A1 |
| GENERAL INFORMATION: US20020146721A1 |
| GENERAL INFORMATION: Berka, Randy M. |
| APPLICANT: Berka, Randy M. |
| TITLE OF INVENTION: Methods For Monitoring Multiple Gene TITLE OF INVENTION: Expression |
| FILE REFERENCE: 10085.500-US |
| CURRENT APPLICATION NUMBER: US/09/974,300 |
| CURRENT APPLICATION NUMBER: 09/680,598 |
| PRIOR APPLICATION NUMBER: 09/680,596 |
| PRIOR PILING DATE: 2001-10-06 |
| PRIOR FILING DATE: 2001-0.66 |
| PRIOR FILING DATE: 2001-0.75 |
| NUMBER OF SEQ ID NOS: 8481 |
| SEQ ID NO 2220 |
| SEQ ID NO 2220 |
| SEQ ID NO 2220 |
| CONTRACT |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (111805)..(113968),(114684)..(115204)
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OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
US-09-754-853A-4
                                                                           Sequence 4, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:
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; ORGANISM: Bacillus licheniformis
US-09-974-300-2320
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US-09-974-300-2320/c
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                                 -09-754-853A-4
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270 AGTATTTCAGCTGCAATAAAGATTGAGTTTGCAATTGTGAGTTCTTTTGCTTCCTCCTGC 329

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1482 CATATTTCTTGGTAGGAAGGCAGCAAACCAGAGGGAGGTAGATCAGGTGCTGGAAGAGT 1541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 TTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTCCTCTAATCCAG 191
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APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
CURRENT APPLICATION UNBER: US/09/887,576
CURRENT APPLICATION UNBER: US/09/887,576
                                                                                                                                                                                                                                                                                                       APPLICANT: HORACITON:
APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-W0
CURRENT PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NOS: 2145
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US-09-880-107-2145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%; Score 32; DB 10; Length 3779; 54.2%; Pred. No. 5; Live 0; Mismatches 55; Indels
330 TGCTGCTACAGAGCAGGGTCTGCTGTGCACCACCTTGGAGAAGG 373
                                                           467 cécircricércaécaéaaccirrririrerrerécareraaaaé 424
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PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR PILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SEQ ID NO 655
                                                                                                                                                                                                                 Sequence 2145, Application US/09880107; Patent No. US20020142981A1; GENERAL INFORMATION:
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Best Local Similarity 54.2'
Matches 65; Conservative
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; LENGTH: 2049
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-655
Query Match 6.3%; Score 31.4; DB 10; Length 204
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Ouery Match
Best Local Similarity 56.2%; Pred. No. 5.7;
Matches 59; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
7 274 TTTCAGCTGCAATAAAGATTGCAATTGTGAGTTCTTTTGCTTCTTCTTCTGCTGCTGCT 333

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Search completed: May 18, 2003, 00:39:58 Job time : 384.517 secs 44, Appl 419, App 14, Appl 14, Appl

Sequence Sequence

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Sequence Seq

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Sequence 28, Application US/09564805

Patent No. 6333403

GENERAL INFORMATION:
APPLICANT: Tavisjain, Sean V.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 28
LENGTH: 26664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | NAME/KEY: misc feature | NAME/KEY: misc feature | LOCATION: (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | (910) | 
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INFORMATION: s at positions 826 and 23180 is G or C; y at INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
INFORMATION: is C or T; n at position 13128 is t or tgat; r at INFORMATION: positions 22211 and 23879 is A or G.
US-08-469-802B-7
US-08-26-803B-7
US-09-453-702B-60
US-09-142-565-5
US-08-761-258-8
US-08-977-306-8
US-08-97-306-8
US-08-9103-931C-3
US-09-103-478-4
US-09-103-478-4
US-08-442-806-1
US-08-442-806-1
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US-09-641-638-419
US-09-656-14
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(cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-08-261-822A-1

US-08-261-822A-1

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US-08-261-81-10

US-09-40-181-10

US-09-579-181-10

US-09-579-181-10

US-09-579-181-10

US-09-579-181-11

US-08-943-731-5

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US-08-943-731-7

US-08-180-31-11

US-08-180-371-11

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Listing first 45 summaries
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Sequence 27, Application US/09564805

Batent No. 6333403

GENERAL INFORMATION:

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Simard, Jacques

APPLICANT: Simard, Jacques

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION NUMBER: US 60/107,468

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PatentIn Ver: 2.0
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                                100.0%; Score 501; DB 4; Length 26664; 100.0%; Pred. No. 6.1e-160; ive 0; Mismatches 0; Indels 0;
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LOCATION: (1)...(228)
OTHER INFORMATION: exon 24
NAME/KEY: polyA_signal
                                                   Best Local Similarity 100.0
Matches 501; Conservative
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LENGTH: 655
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APPLICANT: Taviigian, Sean V.
APPLICANT: Taviigian, Sean V.
APPLICANT: Taviigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NOS: 240
SEQ ID NO SEC ID NOS: 250
LENGTH: 2958
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                                                                                                            1 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT
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Length 655;
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                                                      Indels
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COTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-564-805-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 60.5%; Score 303; DB 4; L
Best Local Similarity 100.0%; Pred. No. 5.1e-93;
Matches 303; Conservative 0; Mismatches 0;
Query Match
60.5%; Score 303; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.1e-93;
Matches 303; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09564805
Patent No. 6333403
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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US-09-564-805-3
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##FILICANI: Simard, Jacques
##FILICANI: Simard, Jacques
##FILICANI: Simard, Jacques
##FILICANI: Simard, Johanna M.
##FILICANI: Rommens, Johanna M.
##FILICANI: Myriad Genetics, Inc.
##FILICANI: Myriad DATE: 1098-11-06
##FILICANI: Myriad DATE: 1998-11-05
##FILICANI: Myriad DATE: 1999-11-05
##FILICANI: Myriad DATE: 1999-11-05
##FILICANI: Myriad DATE: 1004-11-05
##FILICANI: Myriad DATE: 1004-11-05
##FILICANI: Myriad DATE: 1004-11-05
##FILICANI: Myriad DATE: 1004-11-05
##FILICANI: Myriad Myria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC
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Pred. No. 1.6e-76;
0; Mismatches 4; Indels 16;
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Patent No. 5650553
BARBAL INFORMATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION:
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
                                                                                                                                                                                                                           Sequence 225, Application US/09564805
Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.8%;
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Teng, David H.F.
Simard, Jacques
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Best Local Similarity 93.4
Matches 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Gorilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .. (2478)
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                                                               2906 CAA 2908
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; LOCATION: (1)
US-09-564-805-225
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      CAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LANT: Tartigian, Sean V.

Tartigian, Sean V.

APPLICANT: Teng, David H.F.

APPLICANT: Simard, Jacques

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION OF Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION NUMBER: US/09/564,805

CURRENT FILING DATE: 2000-05-05

PRIOR PELICATION NUMBER: 1998-11-05

PRIOR PELICATION NUMBER: 09/434,382

PRIOR PELICATION NUMBER: 09/434,382

NUMBER OF SEQ ID NOS: 240

SOFTWARE: Patentin Ver. 2

SEQ ID NO 223

LENGTH: 2908

TYPE: DARA

ORCAN.
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ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGCCTTTC
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Best Local Similarity
Matches 299; Conserv
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; LOCATION: (1)
US-09-564-805-223
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320 INCCICCIGCIGCIGCIACAGAGCAGGGTC 349
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  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,822
FILING DATE: Une 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3130
                                                              08/261,822
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                         LENGTH: 6042 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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HYPOTHETICAL: N
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PCT-US95-07744A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 TAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTGCAATTGTGAGTTCTTTTGC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618 Trectrigaagaretrgaargestraargagaretriceritrigaratritrecrities 677
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STREET: One Liberty Place, 46th floor
CTTY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Trustees of The University of Pennsylvania
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 17-JUN-1994

CLASSIFICATION: 536

ATTONNEY/AGENT INFORMATION:

NAME: Beardell, Lori V.

REGISTRATION NUMBER: 34,293

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3100
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APPLICATION NUMBER: PCT/US95/07744A FILING DATE: 15-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%; Score 33.2; DB Best Local Similarity 51.3%; Pred. No. 0.67; Matches 77; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCCTCCTGCTGCTACAGAGCAGGGTC 349
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APPLICANT: Trustees of The Universi
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                  ZIP: 19103

COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6042 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                CORRESPONDENCE ADDRESS: ADDRESSE: Woodcock,
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Sequence 1, Application US/08819288

Sequence 1, Application US/08819288

Patent No. 5955652

GENERAL INFORMATION:
PAPLICANT: Alonso, Joseph
APPLICANT: Alonso, Jose
TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
TITLE OF INVENTION: AND PATHOGENS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5955652ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                             200 TICCCIGCACACAGAGACAAGCAGAGIAACAGGAICAGIGGGICIAAGIGICCGAGACI 259
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Query Match 6.6%; Score 33.2; DB 5; Length 6042; Best Local Similarity 51.3%; Pred. No. 0.67; Matches 77; Conservative 0; Mismatches 73; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,288
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-2949
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3139
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Query Match
Best Local Similarity
Matches 77; Conserv
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US-09-149-476-107
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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                                                                                                                                                                            Length 6172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ecker, Joseph
APPLICANT: Alonso, Jose
TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
TITLE OF INVENTION: AND PATHOGENS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/400,348
                                                                                                                                                                                                         73;
                                                                                                                                                                        Query Match 6.6%; Score 33.2; DB 2; Best Local Similarity 51.3%; Pred. No. 0.68; Matches 77; Conservative 0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                     TICCICCIGCIGCIACAGAGCAGGGIC 349
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Patent No. 6355778
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPAN: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                        TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-819-288-1
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LENGTH: 6172 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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US-09-400-348-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                    750 TTCCTTGAAGATCTGAATGCGTAGATCATACGGGATCTTTGCATTTTTGTTGCTTTTCGT 809
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  Score 33.2; DB 4; Length 6172;
Pred. No. 0.68;
0; Mismatches 73; Indels 0;
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EVARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
                                                                                                                                                                                                                                                                         320 TTCCTCCTGCTGCTGCTACAGAGCAGGGTC 349
                                                                                                                                                                                                                                                                                                        870 TTCTTTTGTTGCTGCTTCATACTAAGATC 899
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,333
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
FILING DATE: 1997-05-23
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PLICATION NUMBER: 60/040,163
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FILING DATE: 1997-05-23
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Patent No. 6420526
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milarity 51.3%; F
Conservative 0:
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APPLICATION NUMBER: 60/047,598 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 ARPPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,568 APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 APPLICATION NUMBER: 60/056,662 APPLICATION NUMBER: 60/056,882 APPLICATION NUMBER: 60/056,637 LICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/048,974 APPLICATION NUMBER: 60/043,671 1997-06-06 1997-08-22 1997-08-22 1997-08-22 FILING DATE: 1997-08-22 1997-08-22 1997-04-11 FILING DATE: 1997-08-22 1997-04-11 1997-04-11 1997-04-11 FILING DATE: EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER
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EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER APPLICATION NUMBER: 60/057,650 R APPLICATION NUMBER: 60/056,091
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,815
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,992
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/057,761
R APPLICATION NUMBER: 60/057,761
R APPLICATION NUMBER: 60/057,595
R FILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R PILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,585
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,586
FILING DATE: 1997-05-23 FILING DATE: 1997-06-13 APPLICATION NUMBER: 60/061,060 FILING DATE: 1997-10-02 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11
APPLICATION UNDBER: 60/056,632
ELING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,664 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,875 FILING DATE: 1997-08-22 LICATION NUMBER: 60/057,669 LICATION NUMBER: 60/049,610 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,589 60/047,593 60/047,614 APPLICATION NUMBER: 60/043,670 60/047,501 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 1997-09-05 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-2 EARLIER A BARLIER
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WESOUR 12.
US-09-579-181-10/C

Sequence 10, Application US/09579181.
Sequence 10, Application US/09579181.
GENERAL INFORMATION:
JAPPLICANT: Chrivia, John
JAPPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNFZ Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
FRIOR APPLICATION NUMBER: 60/136,620
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 10
LENGTH: 9354
                                          ö
                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09579181
Batent No. 6365372
GENERAL INFORMATION:
APPLICANT: Chrivia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153.4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ 1D NOS: 17
  Length 2327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 31.2; DB 4; Length 8916; larity 50.7%; Pred. No. 4; Conservative 0; Mismatches 73; Indels 0
                                        Indels
                                        31;
  DB 4;
Query Match 6.2%; Score 31.2; DB Best Local Similarity 35.9%; Pred. No. 1.8; Matches 33; Conservative 28; Mismatches
                                                                                                                                                                               387 AGTGTGGCAGCTGCCTGGTACCCGGGTGGCTT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6780 ACAGGTTTGGGCTGGAGGCGGTGTATGA 6753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver. 2.0
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Best Local Similarity
Thes 75; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-09-579-181-11
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US-09-579-181-10
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SEQ ID NO 11
LENGTH: 8916
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
                                                                                                                                                                                                                                                       7338 receaareceresecacacacaereresecreasecereaaseceaasseariasisae 7279
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                                                                                                                   13 TGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCC 72
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                          DB 4; Length 9354;
                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLOTER: LIMP PC COMPACIDLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INPORMATION:
NAME: DOTLE LEBAY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317,31
                   6.2%; Score 31.2; DE
llarity 50.7%; Pred. No. 4.2;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                7218 ACAGGTTTGGGCTGGAGGCGGTGTATGA 7191
                                                                                                                                                                                                                                                                                                    133 TCAAGGCAGTTTTTAAAGAAGTCTTGGA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROCKOP, DARWIN J.
SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEREDA, LARISA
LARSON, ANDREA W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 200, Application US/08943731
Patent No. 6265157
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PACK, MICHAEL COLIGE, ALAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 787 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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KORKKO, JARMO
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INFORMATION FOR SEQ ID NO:
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Query Match
Best Local Similarity
Ts; Conserv?
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us-09-434-382-28_copy_26164_26664.rni

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Length 20084;

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Query Match
6.1%; Score 30.6; DB 4; 1
Best Local Similarity 52.8%; Pred. No. 10;
Matches 66; Conservative 0; Mismatches 59;
. IUPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-5
                                                                                                                                                                                                                                                                                                                                                                            Db 14188 GTGCA 14184
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CRGANISM: Human
US-09-734-675-3
                                                                                                                                                                                                                                                                                                                                      497 TGACA 501
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APPLICANT: SPOTIAL, LORETTA D.
APPLICANT: SPOTIAL, LORETTA D.
APPLICANT: SPOTIAL, LORETTA D.
APPLICANT: SEREDA, LARISA
APPLICANT: LARSON, ANDREA W.
APPLICANT: COLIGE, ALAIN
APPLICANT: COLIGE, ALAIN
APPLICANT: KORKKO, JAMES
APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
                                                                                               ö
                                                                                                                                                                                                                                             377 TCTGTGCTGTAGTGTGGCAGCTGCCTGGTACCCGGGTGGCTTGGAAGAAGTCAGCTCCCG 436
                                                                                                                                                                    340 TCTGGGCTGAGGCTGGGCACCCAGGAAGGAAGGAAGGTCCCGCACGGGTGCCCGGGACCC 281
                                                                                                                                                                                                                  437 TCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGAGCCACCCTTATTCGCCAAGTCTTTT 496
                                                                                                 Gaps
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0
                                                    6.1%; Score 30.6; DB 4; Length 787; 52.8%; Pred. No. 1.6; tive 0; Mismatches 59; Indels
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CIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,317
REGISTRATION NUMBER: 36,317
REGISTRATION NUMBER: 36,317
REGISTRATION NUMBER: 36,317
RELECOMMULICATION INFORMATION:
TELLEFAK: 215-965-1284
TELLEFAK: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-943-731-5/c
; Sequence 5, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; GENERAL INFORMATION:
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TELEFAX: 811-494
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 20084 base pairs
"VDE: nucleic acid
"VDE: nucleic acid
                                                                                               66; Conservative
                                                                      Best Local Similarity
Matches 66; Conserv
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                US-08-943-731-200
                                                        Query Match
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GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
APPLICANT: WEBSTER, Marion et al
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/09/734,675
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                  Db 14308 TCTGGGCTGAGGGTGGGCACCCAGCAGGAAGGAAGGTGCCCGCACGGGTGCCCGGGACCC 14249
                                                                                                                                                                                                                                                                                                                  Db 14248 TGGGAGTGCCCACTCTGCCCAGTGGTGCTACCCACCCATTCCCGTGTCCTCT 14189
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                                                                                                                                                                                                                                                     437 TCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGAGCCACCCTTATTCGCCAAGTCTTTT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GCAGATGAACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGG 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 38844;
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Best Local Similarity 46.5%; Pred. No. 15;
Matches 99; Conservative 0; Mismatches 114; Indels
Indels
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Job time : 72.1908 secs
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US-09-734-675-3/c
; Sequence 3, Application US/09734675
; Patent No. 6365331
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May 17, 2003, 15:56:54; Search time 1298.06 Seconds (without alignments) 11232.524 Million cell updates/sec 1 ggtatggagctgtgccgagg......trcgccaagtcttttgaca 501 4109280 GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd. 2054640 segs, 14551402878 residues Total number of hits satisfying chosen parameters: US-09-434-382-28_COPY_26164_26664 501 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 gb ba: *
gb ba: *
gb ba: *
gb on: *
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gb ov: *
gb pr: *
gb v: *
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em n: *
em or: *
em pat: *
em pat Minimum DB seq length: 0 Maximum DB seq length: 2000000000 GenEmbl:* Title: Perfect score: Scoring table:

Database :

Sequence:

Run on:

Searched:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ID	AC005277 AF304370 AK074244 BC001939 BC004158	AK094687 AF308698 AX405825 AK094333 AK00122	G60268 AF308694 AF308694 G42927 G42927 AX326639 AX326659 AX326659 AX326659 AX32659	AF429315 MIBMCG MAT450991 AC058799 AC097359 AF429315 AF429315 AC087159 AC01347 AC01347 AC01347	AC004830 AL731655 AC105707 AC1056180 AC126180 AC126082 AC126941 AC10453 AC069268 AC0692567 AC17334 AC117334	118788 bp 1 1 1 hordata; C rimates; C Linton,L.
DB	തെതെതെ	-	н н оо	0	5000000000000000000000000000000000000	omoso 33731 0a; C ia; P 18788 n, K.,
Len	11878 290 216 216 299 300	20902 20908 20908 20908 20908 20908	242 282 288 1389 2989 2083 2083 2083 2083 2083	502 111 111 712 712 811 911 95 95 96 96 96 96 96 96 96 96 96 96 96 96 96	83645 218542 252546 252546 105256 1166386 212386 2125685 1165685 1163685	GI:3 GI:3 GI:3 GI:3 GI:3 GI:3 GI:3 GI:3
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complement (11928...12100)

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9662. 9829
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complement(20553..20
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complement(15320...)
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complement(15838. .1
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  family="AluSx"
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8271. .18311
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complement(5481.
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             Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Barker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Bouwer, K., Brown, A., Castle, A., Cerry, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gardyna, S., Genabelmer, S., Gerapegery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Mohla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                     Direct Submission

Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 3.0 Charles Street, Cambridge, MA 02141, USA

Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Bowon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Garage, D., Gardyna, S., Genshelmer, S., Geragery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Maddonald, P., McGurk, A., McKernan, K., Meltim, M., Morris, W., McGurk, A., McKernan, K., Malla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Nioff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 23, 1998 this sequence version replaced gi:3335015. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Only the first 118.8 kilobases of this clone are being submitted. The remainder overlaps accession number AC005274 (WICGR project L350).
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clone lib="RPCI-11 human BAC library"

95. 884

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1. .118788
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(db_xref="taxon:9606"
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__family="MLT1A1"
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complement (4282. .4321)
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complement (4328. .4608)
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:044. .2076
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/rpt_family="MER34"
/rpt_/rpt_
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complement(3478.
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Direct Submission
Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84108, USA
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KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IELAVRPHSAPEYEDETWTVYQIPIHSEQRRGKHQPWQSPERPLSRLSPERSSDSESN
ENEPHLPHGVSQRRGVRDSSLVVAFICKLHLKRGNFLVLKAKEWGLPVGTAAIAPIIA
AVKDGKSITHEGREILAEELCTPPDPGAAFVVVECPDESFIQPICENATFQRYQGKAD
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DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASLGKPLHPLLVVAPNQLKAWLQQYHNQCQEVLHHISMIPAKCLQEGAEISSPAVERL
ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATL
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/product="putative prostate cancer susceptibility protein
HPC2/ELAC2"
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HPDIFPLLTSFRCKKEGPTLSVPMVQGECLLKYQLRPRREWQRDAIITCNPEEFIVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tavtigian, S. V., Simard, J., Teng, D. H. F., Baumgard, M., Beck, A., Cantigian, S. V., Simard, J. Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnha, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J. S., Hu, R., Iliev, D., Janecki, T., Kort, E. N., Laity, K. E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K. T., Reid, J. E., Richards, S., Schroeder, M., Smith, R., Snyder, S. C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Moodland, A. M., Labrie, F., Skolnick, M. H., Neuhausen, S., Rommens, J. and Cannon-Albright, L. A.
                                           Db 104236 AAGAAGTCAGCTCCCGTCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGAGCCACCCTT 104295
                                                                                                                                                                                                                               2908 bp mRNA linear PRI 23-FF Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 mRNA, complete cds.
                        AAGAAGTCAGCTCCCGTCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGAGCCACCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein_id="AAG24441.1"
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1. .2481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCGCCTTTC
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                                                                                                                                                                                                                                                                                                   note="Single-stranded coverage."
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complement (26912. .26990)
/rpt family="MER21B"
26991. .27290
/rpt family="Alusx"
complement (27291. .27975)
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28034...28197
/rpt_family="LTR28"
28266...28707
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/rpt_family="Lousd"
complement(2597. .25985)
/rpt_family="MLTID"
25816. .2589c
                                                                                                                                                                                                                                                                                                                    complement (25994 . 26099)
/rpt family="purine-rich"
complement (26122 . 26291)
/rpt family="MLTID"
26312 . 26337
                                 rpt_family="L1M4"
'1799. .22104
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28843. .28017
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28920. .29005
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29140. .29233
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LIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAKVPLFSPNFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:chalalema.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA full insert sequencing; 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
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Homo sapiens cDNA FLJ23664 fis, clone HEP03495, highly similar to blative prostate cancer susceptibility protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
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/db_xref="taxon:9606"
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Haiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
George Yang, Scott Zuyderduyn, Marco Marra.
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Submitted (29-030-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1905 aggacrigereccrigecacaecceceeeccaeaecrieccacaeeaaecaaecaaeara 1964
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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CONA Library Arrayed by: The I.M. G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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clone MGC:4102 IMAGE:2820640, mRNA, complete cds.
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                                                                                                                                                                                                                                   Score 301.4; DB 9
Pred. No. 2.4e-92;
0; Mismatches 1
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/clone="HEP03495"
/cell_line="HepG2"
/cell_type="hepatoma"
/clone_lib="HEP"
/note="cloning vector: pl
a 582 c 613 g 43:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Best Local Similarity 99.77
Matches 302; Conservative
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BC004158.1 GI:13278770
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Matches 302;
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AUTHORS
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COMMENT
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                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: i Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MWALCSLLRSAAGRTWSQGRTISQAPARRERPRKDPLRHLRTRE
RRPSGSCGGGPRTVIQVAAGRDSGAALVYBEBRNYLFWCGGGVGRMGBHKLKV
ARLDNIFLTRHWHWSWVGGLSGMILTLKETGLRCVLSGPPQLEKYLBAIKIFGEGPLKG
IELAVRPHSAPEYEDETMTVYQIPIHSEQRRGKHQPWGSPERPLSRLSPERSSDSELN
BENPHULPRGVQRRGYRDSSLVVAFICKLHLKRGMFLVLKARBMGLPVGTAALAPITA
AVKDGKSITHEGREILLAELCTPPPDPQAARTVVVECPDBSFIQPICGRATGRATAIA
APVALVVHMAPASVLVDSRYQQWMERFGPDTQHLVLNBNCASVHNLRSHKIGTQLNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPDIFPLLTSFRCKKEGPTLSVPMVQGECLLKYQLRPRREWQRDAIITCNPEEFIVBA
LQLPNFQQSVQEYRRSAQDGPAPAEKRSQYPEIIFLGTGSAIPMKIRNVSATLVNISP
DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASLGKPLHPLLVVAPNQLKAWLQQYHNQCQEVLHHISMIPAKCLQEGAEISSPAVERL
ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTWPCEALVRMGKDATL
LIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNFSQRYAKVPLFSPNFS
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                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/produc="butative prostate cancer susceptibility protein"
/protein_id="AAH10399.1"
/db_xref="GI:12804973"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2786 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGGCACCTTTC
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                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="LocusID:60528"
/db_xref="Laxon:9606"
/dlone="MGC:4102 IMAGE:2820640"
/tissue type="Lung small cell carcinoma"
/lab_host="NHH MGC_7"
/note="NULOBER"
/note="Uvector: pOTB7"
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Pred. No. 2.6e-92;
0; Mismatches 1;
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Best Local Similarity 99.7%;
Matches 302; Conservative
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PRI 12-JUL-2001

BC004158 3006 bp mRNA linear PRI 12-JUL Homo sapiens, putative prostate cancer susceptibility protein, clone MGC:2441 IMAGE:2820640, mRNA, complete cds.

LOCUS

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/translation="MWALCSLLRSAAGRTWSQGRTISQAPARRERPRKDPLRHLRTRE

KREPSGCGGGORTUTVLQVVAAGSRDSGAALVYBERRNILFRGGGOVGLMOHGMGHKLKV

ARLDNIFLTRHUMSWUGGLSGHLTTLKETGLPKCULSGPPQLEKYLEAIKIFSGPLKG

IELAVRPHSAPEYEDETWTVYQIPIHSEQRRGKHQPWGSPERPLSRLSPERSSDSELN

BUNEPHLHPGWSQRRGYNDSSLVVAFTCKHLKKGMFPLVLKAKRGALPVGTAALAPIIA

AVKDGKSITHEGREILLAELCTPPPDPGAARVVVBCPDESFTQPICTAATATAPIIA

APVALVVHMAPASVLVDSRYQQWMERPGPDTQHLVLNBNCASVHNLRSHKIQTQLNLI

HDDIPPLIFSRRCKKEGPTLSVPWYQGECLLKYQLRRPREWORDAIITGNPERFIYBA

LQLPNFQQSVQBYRSAQDGCAPASKRSQYPEIIFGTGSAIPMKRNVSFAILVNISP

DTSLLLAGGEGTFGQLCRHYGDQVDRVLGTLAAVFVBHLHADHHTGLPSILLQRERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: c Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621.

Location/Qualifiers
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LIHBATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAKVPLFSPNFS
EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSRE
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// Codon_start=1

// product_=rgutative prostate cancer susceptibility protein"

// protein_id="MAH04158.1"

// db_xref="GI:13278771"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 3006)
Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                            Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2675 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 2734
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'clone lib="NIH MGC 7"
'lab host="DH10B-R"
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                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contal: cgapbs.r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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/db_xref="LocusID:60528"
/db_xref="taxon:9606"
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Direct Submission

L Submitted (04-UJU-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; DNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA ilbrary
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation; HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                           194687 2907 bp mRNA linear PRI 15-JUL-2002 to sapiens cDNA FLJ37368 fis, clone BRAMY2024530, highly similar Homo sapiens prostate cancer susceptibility protein HPC2/ELAC2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                   2795 ACTAATTTCATTTCAAGGCAGTTTTTTAAAGAAGTCATGGAAACAGACGGCGCGCCCTTTC
                                                                                                                                                                   2855 CTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTG
                                                         121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC
                                                                                                                                       CTCTAATCCAGCAAAGTGATTCCCTGCACACAGAAGAAGCAGAGTAACAGGATCAGTG
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Homo sapiens amygdala cDNA to mRNA, clone_lib:BRAMY2
clone:BRAMY2024530.
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/clone_lib="BRAMY2"
/note="cloning vector: pME18SFL3"
788 c 839 g 584 t
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Pred. No. 1.3e-91;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone="BRAMY2024530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens cDNA FLJ37368 fis,
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AK094687.1 GI:21753794
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Best Local Similarity 99.7%;
Matches 300; Conservative
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JOURNAL
REFERENCE
AUTHORS
                                                                                                                                       181
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JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Pan.

Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

I (bases 1 to 2908)

Tavtigian, S. V., Simard, J., Teng, D. H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N. J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Franham, J. M., Franh, D., Frye, C., Ghaffari, S., Gupte, J. S., Hu, R., Illev, D., Janecki, T., Kort, E. N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A. M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p E 2105527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outputs...e. 1 to 2908)

Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Dayananth, P., Destrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Iaity, K., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pedestron, A., Denn, B., Peterson, K.T., Reid, J.E., Richards, S., Troceder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A. M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
Submission
Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
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(bases 1 to 2908)

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2 (bases 1 to 2008)

Destroidand, S.V., Jeng, D.H.F., Baumgard, M., Dayananth, P., Destroiders, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Leavitt, A., Lebbanc, G., MoArthur-Morrison, J., Pederson, A., Penn, B., Beterson, K.T. Swedlund, B., Swensen, J., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Tromas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Pan troglodytes ortholog of human HPC2/ELAC2

Uppblished
2607 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT
                                                                                                                                                      121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCGCCTTTC
                                                                                                                                                                                                                                                                                                             241 GGTCTAAGTGTCCGAGACTTAACGAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG
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AF308698
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Homo sapiens
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     HYSEQ,
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Matches 299;
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/product="ELAC2"
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/protein_id="AAG24920.1"
/protein_id="I0946497"
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KRGPSGCSGGPNTVYLOVVAAGSRDSGAALYVFSEFNRYLFNCGEGIORLMQEHKKV
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Novel nucleic acids and polypeptides
Patent: WO 0222660-A 240 21-MAR-2002;
                                                                                                                                                                                                                                                                                                      ARLDNI FLTRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEAIKI FSGPLKG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                db_xref="taxon:9598"
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/translation="WWALCSLLRSAAGRTWSQGRTISQAPARRERPRKDPLRHLRTRE
KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKV
ARLDNIFLTRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                          IELAVRPHSAPEYEDETMTVVQIPIHSEQRRGKHQPWQSPERPLSRLSPERSSDSESN
REPHLAPROGRRGYRDSSLVVAFTCHLHKRGFLVLKARMGLPVGTAALABIIA
AVNDGKSITHEGREILLAEELCTPPDFGGARVVVCEDFDSFIQD; TGRATFORYGKAD
APVALVVHMAPASVLVDSRYQQWMERFGPDTQHLVLNENCASVHNLRSHKIGTQLNLI
HPDIPPLLTSRCKKGFPTLSVPWYGGBCLLKYQLRRREWGRAAIITORPEEFIVEA
L\QLRRFQGSVQEYRRSAQDGPABEKRSQYPEIIFGTGTGAAP
I\QLRRFQGSVQEYRRSAQDGPABEKRSQYPEIIFGTGSAIPMKIRNVSATLNNISP
DISLLLDGGGGTFGGLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
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ISLLRTCDEEPQTCLVRHKCHAFGACALUHTSGWKVYSGDTMPCEALURMGKOATL
LIHEATLEBGLEEEBAVEKTHSTTSQAISVGNRNNABEIMLNHFSQRYAKVPLFSPPPS
EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSRE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                      /note="unnamed protein product"
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                                                                                                                                                                                                                                                        /protein_id="CAD34932.1"
/db_xref="GI:21439090"
                                                                     organism="Homo sapiens"
                                                                                                    db_xref="taxon:9606"
Location/Qualifiers
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AK001392
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                                                                                                                                                                                                   Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) Whord to DNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA full insert sequencing: construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Mamanoto,J., Isono,Y., Kawai-Hio,Y., Saito,K. Nishikawa,T., Kimura,K., Yamashite,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Yazhabashi-Teyjii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Naqahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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highly similar
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AKO94012
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Homo sapiens uterus cDNA to mRNA, clone_lib:UTERU2
clone:UTERU2008901.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 294.6; DB 9;
Pred. No. 5.7e-90;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="cerebellum"
/clone lib="BRACEE"
/note="cloning vector: pME18SFL3"
708 c 724 g 631 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Homo sapiens"
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/clone="BRACE2010203"
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1. .2734
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Isogai,T. and Yamamoto,J.
Direct Submission
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamateari, Kisarazu, Chiba 292-0812, Japan (64-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamateari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NBDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA inbrary construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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                                                                                                          Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamanoto, J., Isono, Y., Kawat-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanchori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T., Sugano, S., NEDO, human, CDNa, sequencing project
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens cDNA FLJ10530 fis, clone NT2RP2000985.
AK001392
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/tissue type="uterus"
/clone_lib="UTERU2"
/note="cloning vector: pME18SFL3"
754 c 806 g 623 t
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Pred. No. 5.7e-90;
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/organism="Homo sapiens"
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Local Similarity 98.7%;
les 297; Conservative (
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Direct Submission
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Homo sapiens.
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G60268/c
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S Isogai, T. and Otsuki, T. Direct Submission

Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5- & 3-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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AVKDGKSITHEGRELLAEELCTPPDDPGAAFVVVECPDESFIQPICENATFQRYQGKAD
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HPDIEPLLTSRRCKEGPFLSPHVQGECLLKYQLPRREWGNDAITVRDEEFVDAL
QLPNIPQOSVOBYRRAAAQDGPAPAEKASQYPEIIFLGTGSAIPMKIRNVSATUNNISP
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IHEATLEDGLEEEAVEKTHSTTSQAISVGMRNNAEFIMLNHFSQRYAKVPLFSPNFSBI
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                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/db_xref="taxon:9606"
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/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA)
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AK001392.1 GI:7022621
oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
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/note="unnamed protein product"
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                                                                                 ib:NT2RP2 clone:NT2RP2000985.
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                                                                                    clone_lib:NT;
Homo sapiens
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human sequence in NCBI. STSs designed and developed at the Human Genome Center.
Location/Qualifiers
1. .429
/organism="Homo sapiens"
/db_refe="taxon:9606"
/map="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                  G60268 11near STS 30-MAR-2000 SHGC-130964 Human Homo sapiens STS genomic, sequence tagged site.
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                                                                                                                                                                                                     2856 CTCTAATCCAGCAAATGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGATCAGTG
                                          121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGCCCCTTTC
                                                                  2796 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGGCGCCCTTTC
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94 degrees C for 30 s
60 degrees C for 30 s
72 degrees C for 23 s
30
Perkin Elmer 9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
AmpliTag Gold Polymerase: 0.07 units/ul
Total Vol: 5 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA
Tel: (650) 320-5800
Fmax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: TTTGCTGGATTAGAGGAAAGGTG
Primer B: AGTGAAGATCTGGAGAAGGTG
Primer B: AGTGAAGATCTGGAGAACCTGAA
STS size: 322
PCR Profile:
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Gorilla gorilla.

Gorilla gorilla.

Gorilla gorilla.

Gorilla gorilla

Gorilla gorilla

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Gorilla.

I (Dases 1 to 2893)

I (Dases) 1 to 2893)

I (Camp, N. V. Simard, J. Teng, D.H.F., Abtin, V. Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Gamp, N.J., Garillo, A.R., Tenn, D.W., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iilev, P., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Santh, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchart, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p 21095977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tavidian, S. V., Sharard, J., Teng, D. H. F., Baumgard, M., Beck, A., Tavidian, S. V., Sharard, J., Teng, D. H. F., Baumgard, M., Beck, A., Davananth, P. Desrochers, M., Dumont, M., Farhlam, J. M., Frank, D., Frye, C., Ghaffari, S., Gupte, J. S., Hu, R., Iliev, D., Janecki, T., Kort, E. N., Laity, K. E., Peterson, K. T., Reid, J. E., Richards, S., Schroeder, M., Smith, R., Snyder, S. C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A. M., Labrie, F., Skolnick, M. H., Neuhausen, S., Rommens, J. and Cannon-Albright, L. A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 300
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Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, F., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S.,
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                                                                                                                                                                                                                         1 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT
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H
                                                                                                                                              DB 11; Length 429;
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                                                                                                                                                                                    Indels
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                                                                                                                                              Score 286.4; DB 11;
Pred. No. 2.4e-87;
0; Mismatches 1;
                                                                                   115 t
                                                                .427)
/clone_lib="Human"
106. .427
106. .128
complement (405. .42
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                                                                                   108
                                                                                                                                              57.2%;
                                                                                   115 c
                                                                                                                                              Query Match 57.2
Best Local Similarity 99.3
Matches 298; Conservative
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REFERENCE
AUTHORS
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AUTHORS
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JOURNAL
MEDLINE
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JOURNAL
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SOURCE
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ORIGIN
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VRLDNI FLTRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEÄIKIFSGPLKG
IELAVRPHSAPEYEDETMTVVQI PIHSEQRRGRHQPWQSPERPLSRLSPERSSDSESN
BENEPHLPHGVSQRRGYRDSSLVVAFICKLHLKRGNFLVLKAKEMGLPVGTAAIAPIIA
AVKDGKSI THEGRE ILAELCTPPDPGAAFVVVCCPDESFI OPI CENATFQRVGKAD
APVALVVHMARESVLUVDSRYQQWMERFGPDTQHLVLNENCAS'HNLRGHKI OYGLMI
HPDI FPLLTSFPCKKEGPTLSVPWVQGECLLKYQLRPRREWQRDAI ITCNPEEFI VEA
LQLPNFQQSVQEYRRSVQDVPAPABEKRSQYPEI IFIGTGSAI PMKIRNVSATIVNI SP
                                                                                                                                                                                   Direct Submission
Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84103, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLLNILLQREQAL
ASLGKPLHPLLVVAPSQLKAWLQQYHNQCQEVLHHISMIPAKCLQEGAEISSPAVERL
ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATL
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EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSGE
LAGGLEDGEPQQKRAHTEEPQAKKVRAQ"
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KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 25-JAN-2001
Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="similar to Homo sapiens HPC2/ELAC2"
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Pred. No. 4.1e-76;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                    /organism="Gorilla gorilla"
/db_xref="taxon:9593"
1. 2893
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Sequence 42 from Patent WO0102568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAG24916.1"
/db_xref="GI:10946489"
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/product="ELAC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="ELAC2"
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/gene="ELAC2
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ilarity 93.4%;
Conservative
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Query Match
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                                                                        SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 386)
Milliams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
Lamson, G., Dranac, R., Crkenjakov, R., Drmanac, S., Dickson, M.,
Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B.
Human genes and gene expression products
CHIRON CORPORATION (US); HYSEQ, INC. (US)

Location/Qualifiers
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Bukaryotta.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(base) 1 to 137)

Mang, D.G., Fan, J.B., Siao, C.J., Berno, A., Young, P., Sapolsky, R., Ghandour, G., Perkins, N., Winchester, E., Speneer, J., Kruglyak, L., Stein, L., Hsie, L., Topaloglou, T., Hubbell, E., Robinson, E., Nutsbaum, C., Rozen, S., Shen, N., Kilburn, D., Rioux, J., Nusbaum, C., Rozen, S., Hudson, T.J., Lipshutz, R., Chee, M. and Lander, E.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            042927
WIAF-176-STS Human THudson EST Homo sapiens STS cDNA, sequence
tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACCCGGGTGGCTTGGAAGAAGTCAGCTCCCGTCGTAGTGAGCACCTCTGGAACCTGTC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTACCCGGGTGGCTTGGAAGAAGTCAGCTCCCGTCGTAGTGAGCGACCTCTGGAACCTGTC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900 Fax: 617 252 1902 Fax: 617 252 1902 Fax: 617 ATATGGAGCTGAAATACTATTTCG FINER B: AAGTCATGGAACAGACGCTGTAATACTATTTCG FINER B: AAGTCATGGAACAGACGGCTATTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 6.3e-43;
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100.0%; Pred. No. c...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       103
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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AX069570
AX069570.1 GI:12579355
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0
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Best Local Similarity 100.
Matches 158; Conservative
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                                                                 human.
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                                                           SOURCE
ORGANISM
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JOURNAL
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PUBMED
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AUTHORS
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G42927/c
ACCESSION
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                                         KEYWORDS
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                                                                                                  PCR Cycles:
30 _____Thermal Cycler: custom built by IAS, Costar, Cambridge MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 CCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACGAAAATA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AAGTCATGGAAACAGACGGCGGCACCTTTCCTCTAATCCAGCAAANTGATTCCCTGCANA 78
                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Human THudson EST"
//note="STSs derived from sequences in dbEST and the Unigene collection."
                              94 degrees C for 4.00 minutes 94 degrees C for 50.0 seconds 58 degrees C for 1.50 minutes 72 degrees C for 1.00 minutes 30
                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/map="36.40 cR from top of Chr17 linkage group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 133.4; DB 11; Length 137; Pred. No. 1.5e-34; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 t
                                                                                                                                                                                                                                                                                                                                                             1. .137
/organism="Homo sapiens"
                                                                                                                                                                       Μď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (118. .137)
                                                                                                                                                    10 ng
each 5 p
4 nM
0.5 U
20 uL
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                     1.5 mM
50 mM
10 mM
                                                                   Annealing:
Polymerization:
                                                   Denaturation:
                                                                                                                                                                                                     Taq Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.6%;
97.8%;
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Matches 134; Conservative
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                                 Presoak:
                                                                                                                                                                                                                                                                                                       Tris-HCl:
Gelatin:
                                                                                                                                                    Template:
size: 137
Profile:
                                                                                                                                                                       Primer:
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Mg2+:
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                                                                                                                                      Protocol:
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primer bind
BASE COUNT 2
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OM nucleic -

Run on:

Seguence:

Database

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AZ756633 ev14b07.1

AQ378798 RPC111-15

AA684125 no.109608.8

AA6843719 DKFZ6434L

BW55850 AGENCOURT

BC614109 1103909.X

BF913236 113.47011

AQ05225 HS. 3037 A

AG01322 Homo sapi

AG01322 UavdfC1.Y

BF589079 nac29h02.

AI821670 zud0fC1.X

AQ144748 HS. 3092 A

AQ19249 CIT-HSP-2

AQ583832 RECI-11-4

AG059314 Pan trog1

BF34266 602013777
                                                                                                           AQ628850 RPCI-11-4
AQ086239 HS 2171 B
AQ183714 HS 3205 B
AQ343449 RPCI11-12
AQ740452 HS 5502 A
AG677233 HS 5522 A
AL696113 DKFZD686A
B44892 HS-1060-A1-
AL707132 DKFZD686A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              br244530
601862835F1 NIH_MGC_57 Homo sapiens CDNA clone IMAGE:4080393 5',
mRNA sequence.
             AC09972 EL78610.x
AQ196057 RPC111-58
AQ071874 HS 3018 A
AG084157 Pan trog1
AQ230437 HS 2034 A
B95260 CIT-HSP-217
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11H-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM940 row: f column: 10
High quality sequence stop: 328.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                         AQ677233
AL696113
B44892
AL707132
AZ756633
AZ756633
AZ756633
AZ75683
AZ584125
AZ584125
BMS58580
BQ614109
BQ614109
BQ614109
AQ996225
AQ96222
                                                                                                                                                                                                                                                                                                                                                                                                    A1820920
BF589079
A1821670
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AQ583832
AG059714
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1115.6
1115.6
1115.4
1115.4
1115.2
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1115.2
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AUTHORS
TITLE
JOURNAL
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BG943515 ax38g05.x
AG177687 Pan trogl
AQ742365 HS 5382_B
AQ587593 CITBI-EI-
AQ587553 CITBI-EI-
                                                                                           May 17, 2003, 15:56:54 ; Search time 680.481 Seconds (without alignments) 11900.029 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                           1 tatcaggtgactgaattcta......aagctctgagggactgacgt 500
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version 5.1.5
- 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                       16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             nucleic search, using sw model
                                                                                                                                                     US-09-434-382-28_COPY_1_500
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BG943515
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AQ742365
AQ587593
AQ587553
                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
GenCore
Copyright (c) 1993
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gb_htc:*
gb_htc:*
gb_est4:.*
gb_est5:*
em_est6m:.*
em_est6m:.*
em_gss.*:
em_gss_inv:.*
em_gss_inv:.*
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em_gss_fun:*
em_gss_mam:*
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Maximum DB seq length: 200000000
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em_gss_other
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em_estin: *
em_estov: *
em_estpl: *
em_estpl: *
em_ettpl: *
em_ttc: *
gb_estl: *
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Match
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23.9
23.6
23.6
23.6
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1119.6
1118.2
1118.2
1117.8
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Result No. υ

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(bases 1 to 669)
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Matches 140; Conserv
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KEYWORDS
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AG177687
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                                            /clone='InAds: 4veu.>>
/clone='InAds: 4veu.>>>
/clone='InAds: 4veu.>>>
/clone='InAds: 4veu.>>>
/tissue_type="glioblastoma"
/lab_host="NIHH MGC_57"
/lab_host="DH10B (TI phage-resistant)"
/note="organ: brain; Vector: pDNR-LIB (clontech); Site_I:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
and 3' adaptors were used in cloning as follows: S'
adaptor sequence: S'-ARGGCGCATTATGGCC.3' and 3' adaptor
sequence: S'-ATTTAGAGGCCGAGGCGCCACATG-dT(SN 3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG943515 546 bp mRNA linear EST 11-JUN-2001 ax38905.x1 Proliferating Human Erythroid Cells (LCB:ax library) Homo sapiens cDNA clone ax38905 random, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9817, National Institutes of Health, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases I to 546)
Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="ax38g05"
/clone_lib="Proliferating Human Brythroid Cells (LCB:ax
library)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TTTTTGTTTTGTTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCGATTCTCCTGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 TTTTTTTTTTTTTTTTTTTTTTTTTTGGACACAGAGTCTCGCTCTGTCGCGCAGGCTGGAGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: jm7f@nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 38 row: g column: 05
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 GCAGTGGGGGGGATCTCGGCTCACTGCAACCTCTGCCTCCGAGTTCAAGCGATTCTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.5%; Score 122.4; DB 12; Length 992; 84.1%; Pred. No. 1e-13; ive 0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crcagccrccrgagragcrgggarracaggcgcgcgcgccaccacg 146
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/organism="Homo sapiens"
/db_xref="taxon:9606"
organism="Homo sapiens"
                     'db_xref="taxon:9606"
'clone="IMAGE:4080393"
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Fax: 301 435 5148
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/incte="Organ: blood; Vector: Lambda ZAP II; Site 1: ECORI; Site 2: ECORI; 65,000 proliferating erythroid cells from the buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIzol reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's Caprinder CDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda Zap II weetor (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center http://www.nisc.nih.gov/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Pan troglodytes DNA, clone: RP43-049G22.TJ, genomic survey
                                  /cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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BAC end sequences of Library RPCI-43
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 CTCGGCCTCCCGAGTAGCTGGGATTACACAGGTGTGCCACCATGCCCAACTAAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 119.6; DB 1
Pred. No. 4.3e-13;
0; Mismatches 34
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type="blood"
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80.5%;
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Gaps

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DB 17; Length 811;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eukaryota; Eto 399)

I (Dases 1 to 399)

S Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

Unpublished (1997)

Other (285s: CITELE-1-2643H8.TF

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

184 c 170 g 248 t 43 others
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Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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                                                                                  1. .811
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="plate=958 Col=15 Row=D"
/clone=lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.6%; Score 118.2; DB 17; Length ilarity 70.0%; Pred. No. 6.9e-13; Conservative 0; Mismatches 73; Indels
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-388
Tel: (206) 616-388
Tel: (206) 616-3887
Email: jwallacc@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web_Server:
Plate: 958 row: D column: 15
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Adams, M.D. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 811)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. ar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 CAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
| 146 c 130 g 233 t
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                                                                                                                                                                                                                                                             l. .669
/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9598"
/clone="RP43-049G22.TJ"
                                                                                                                                                                                                                   Location/Qualifiers
                                                                                  : pBACe3.6
: EcoRI
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DNA linear GSS 07-JUN-1999 sapiens genomic clone 2643HB, DNA

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AU121896 AAMMAI Homo sapiens CDNA clone MAMMAI001220 5', mRNA
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 727)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bmail: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                  339 TITITITITITITITITITITITITITIGAGAIGGAGICTICCICCICCACCAGGCIGGAGIGCAG 280
                                                                                                                                                                CTCTTGCTTTAGAGCTTGTCCTCTATTCTTGCTTTTCCAAAAAACACTACAATTTT 184
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                                                                                                                                                                                                                                                                                                                                 TGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTT-AAGCGATTCTCTCCTGCCTC 303
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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Pred. No. 8.6e-13;
                                                                                 23.6%; Score 117.8; DB 73.8%; Pred. No. 1e-12;
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/tissue_type="mammary gland"
/note="Vector: pME185FL3"
159 c 146 g 248 t
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/clone="MAMMA1001220"
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ilarity 73.8%;
Conservative 0
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Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-438-52-3975
Fax: 81-438-52-3986
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CalTech F
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1 (Bases 1 to 450)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQS87553 450 bp DNA linear GSS 07-JUN-1999
CITBI-E1-2643H14.TR CITBI-E1 Homo sapiens genomic clone 2643H14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Other GSSs: CITBI-E1-2643H14.TF
Other GSSs: CITBI-E1-2643H14.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                     /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
83 c 108 g 89 t
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/organism="Homo sapiens"
/db xref="taxon:9606"
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/sex="male"
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73.8%;
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Best Local Similarity 73.8
Matches 163; Conservative
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TGTTTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCCAGGCTGGAGTGCAG

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Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                              AI609972 415 bp mRNA linear EST 21-APR-1999 tt78c10.x1 NCI CGAP HSC3 Homo sapiens cDNA clone IMAGE:2246898 3' similar to contains Alu repetitive element; contains element MER9 repetitive element; mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 415)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: bone marrow; Vector: pAMP1; mRNA made from pymphoid tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2246898"
/clone=lib="NCI_CGAP_HSC3"
/tissue_type="CD34+, T negative, patient with chronic myelogenous leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 ACACTACAATTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCA 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTCCTGCCTCAGCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCAC 343
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304 AGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                        150 AGCCTCCTGAGTAGCTGGGATTACAGGCGCGCGCCACCACG 110
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0; Mismatches 34
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AIG09972.1 GI:4619139
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Best Local Similarity
Matches 138; Conserv
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AQ196057/c
LOCUS
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AI609972/c
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/coll_type="chimeric hamster somatic cell hybrid"
/coll_type="chimeric hamster somatic cell hybrid"
/note="wycotor: soco-1; Human Chromosome 11 specific cosmid
library prepared from flow sorted human Chromosome 11
derived from Chinese Hampster Ovary (CHO) monochromosomal
somatic cell hybrid, J1"
169 c 185 t 31 others
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria)

1 (bases 1 to 770)

Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M., Jones, D., Ward, T., Gillian, E., Schageman, J., Probst, S., Harris Garner, H., M., Probst, S., Harris Garner, H.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B02308 13-JUL-19 CSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-151D1, DNA sequence.
                                                            431
                                                                                                                             303
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Location/Qualifiers
1. 770
| /organism="Homo sapiens" / db_xref="taxon:9606" | /clone="cSRL-151D1" /clone_Ib="cSRL flow sorted Chromosome 11 specific
                           TGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTT-AAGCGATTCTCCTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic Sequence Sampled Map of Chromosome 11
Unpublished (1996)
Contact: Evans GA, Shane Probst
MCDermott Corn Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
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Pred. No. 8.4e-13;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                   304 AGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                                                                                                     BACKWARD: CTTTCTCTACCAGGAAGGAC
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Best Local Similarity 83.2%;
Matches 134; Conservative
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                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 669)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Unpublished (1998)
Other_GSSs: RPCIII-58G11.TK
                                                                                                                                                                                                                                                                                                                                                                                                            Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 389)
RPCI11-58G11.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-58G11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sch_ruzz_
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
126 c 145 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 TAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 TTGCCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAACCTCGGCCTTCCGGGT 301
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                                                                                                                                                                                                                                                                                           Contract: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="GDB:7522042"
db_xref="taxon:9606"
clone="RPCI-11-58G11"
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'sex="Male"
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AQ071874.1 GI:3390723
                                                         AQ196057.1 GI:3607669
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                        sednence.
                                                                                                                  Homo sapiens
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Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 03-NOV-2001
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Pan troglodytes DNA, clone: PTB-081N03.F, genomic survey sequence.
AG084157
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .389
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/clone="Plate=3018 Col=10 Row=1"
/clone="Plate=3018 Col=10 Row=1"
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH10B"
115 c 87 g 118 t
                                                                                Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 AGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTTCGCGCTTAAGCGATTCTCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 AGTGCAGTGGTGCGATCTTGGCTCACGGCAAACTCCGCCTCCCGGGTTGCGCCATTCTCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 CAATTTTTGTTTTGTTTTGTTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGG 237
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23.5%; Score 117.4; DB 17; Length 389;
Best Local Similarity 81.4%; Pred. No. 1.3e-12;
Matches 136; Conservative 0; Mismatches 31; Indels 0;
                                                                                                               scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                USA
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                             Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 389.
Location/Qualifiers
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Plate: 3018 row: I column: 10
Class: BAC ends
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 312)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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HS_2034_A2_F03_MR_CIT_Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=6 Row=K, DNA sequence.
AQ230437

GSS_55666

GSS_655666
Clones are derived from the chimpanzee BAC library PTB This BAC was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                        348 chacciciccanacchacantraagrachinininininininininingeagang 289
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                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L, Halp Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA TEL: (206) 616-3887 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                            47;
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                                                                                                                                                                    1. .654
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Plate: 2034 row: K column: 6
Class: BAC ends
                                                                                                                                                Location/Qualifiers
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                                                                                                   Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                     Sequencing: -21M13
                                      clone tracking errors.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaliai Eutheria; Primates; Catarrhini; Hominidae; Homo.

18 Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1988)

VL Unpublished (1998)

VL Unpublished (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998 UP5260 18 18 DNA linear GSS 26-JUN-1998 CIT-HSP-2171L9.TR CIT-HSP Homo sapiens genomic clone 2171L9, DNA sequence.
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Seg primer: M13 Reverse
Class: BAC ends.
1. .312
/organism="Homo sapiens"
/dr Aref="txxxn:960"
/db Aref="txxxn:960"
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/sex="male"
/note="male"
/note="norgan: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
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/organism="Homo sapiens'
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/db_xref="taxon:9606"
/clone="2171159"
/clone=1ib="CIT-HSP"
/sex="Male"
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B95260.1 GI:2977597
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Matches 151; Conservative
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Search completed: May 17, 2003, 18:18:14
Job time : 687.481 secs
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RPCI-11-479118.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-479118
, DNA sequence.
AQ628850.1 GI:5091242
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieters@dejong, med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 418)
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/note="Vector: pBACe3.6; Site 1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
84 7 78 9 153 t
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                    1;
                                                                                            Length 389;
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Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                  41; Indels
                                                                                          DB 17;
                                                                                          Score 116.4; DB 1
Pred. No. 1.9e-12;
                                                                                                                                  0; Mismatches
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1. 418

Organism="Homo sapiens"

/db_xref="GDB;7683761"

/db_xref="taxon:9606"

/clone="RRCI-11-479118"

/clone lib="RPCI-11"

/sex="Male"
                                      119
                                  82 g
                                                                                            23.3%;
78.4%;
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Best Local Similarity 78.4
Matches 152; Conservative
                  HindIII"
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                                     Gaps
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 DB 17; Length 418;
                                   Indels
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                                                                                                                                                                                                                                       287 GCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCGCGCCCACG 332
                                     31;
Score 116.4; DB 1
Pred. No. 1.9e-12;
0; Mismatches 31
 23.3%;
81.3%;
Query Match 23.3
Best Local Similarity 81.3
Matches 135, Conservative
                                                                         179 AATTTTTTTTTTTTTTTTTTT
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Sequence 1404, Ap Sequence 1404, Ap Sequence 1404, Ap Sequence 7825, Ap Sequence 7, Appli Sequence 1076, Ap

Sequence 1077, Ap Sequence 1077, Ap

Sequence 9422, Ap

Sequence 3, Appli Sequence 86, Appl Sequence 90, Appl Sequence 3132, Ap Sequence 87, Appl Sequence 91, Appl

Sequence 3133, Ap Sequence 326, App Sequence 327, App

Sequence 326,

Sequence 9139,

Sequence 715, Sequence

Sequence 327 Sequence 327

Run on:

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APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sand H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT FILING DATE: 2001-11-20
RIOR APPLICATION NUMBER: US 60/107, 468
PRIOR APPLICATION NUMBER: US 60/107, 468
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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LOCATION: (9107..(13104)
COTHER INFORMATION: exon 1: 3105-3089; exon 3:
OTHER INFORMATION: exon 6: 582-5650; exon 7: 7075-7194; exon 8:
OTHER INFORMATION: exon 6: 582-5650; exon 7: 7075-7194; exon 8:
OTHER INFORMATION: 13032-13104;
NAME/KEY: misc feature
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US-09-795-68-1404
US-09-798-68-1404
US-09-798-029-7
US-10-074-095-1076
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US-09-946-801-332
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US-09-795-668-327
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US-10-091-572-715
US-10-091-572-715
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SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 26664
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Sequence 8719, Ap
Sequence 78, Appl
Sequence 146, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 11, Appli
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                                                                                 May 17, 2003, 17:27:39 ; Search time 63.3902 Seconds (without alignments) 10174.595 Million cell updates/sec
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Sequence 28, Appl
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-764-891-8719
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US-09-954-531-146
US-10-237-859-3
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US-10-091-438-263
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APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Ryriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION NUMBER: US/09/988,687
CURRENT APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
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             OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23: 0THER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation OTHER INFORMATION: signal: 26447-26452

NAME/KEY: variation
LOCATION: (826).. (23879)
OTHER INFORMATION: positions 826 and 23180 is G or C; y at OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486 OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at OTHER INFORMATION: positions 22211 and 23879 is A or G.
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                                                                                                                                                                                                                                  100.0%; Score 500; DB 9; Length 26664; 100.0%; Pred. No. 1.3e-131;
                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/09988687
Publication No. US20030045704A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                       Similarity
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US-09-988-687-28
                                                                                                                                                                              OTHER INFORM
US-09-988-626-28
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                       Local
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OTHER INFORMATION: 25026-2.2.
OTHER INFORMATION: signal: 26447-26432.
OTHER INFORMATION: signal: 26447-26432.
OTHER INFORMATION: signal: 26447-26432.
INAME/KEY: variation
LOCATION: (826). (23879)
OTHER INFORMATION: sat positions 826 and 23180 is G or C; y at OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
OTHER INFORMATION: positions 22211 and 23879 is A or G.
OTHER INFORMATION: positions 22211 and 23879 is A or G.

COTHER INFORMATION: positions 22211 and 23879 is A or G.

OTHER INFORMATION: positions 22211 and 23879 is A or G.
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  09/434,382
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PRIOR APPLICATION NUMBER: 09/v
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                       sapiens
                                                                                                                            TYPE: DNA
ORGANISM: Homo
                                                                                  SEQ ID NO 28
LENGTH: 26664
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LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g or
                          COCATION: (1).7.(1531)

THER INFORMATION: y=t/u or c
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LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
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                                                                                                         LOCATION: (1)...(1531)

THER INFORMATION: m=a or FEATURE:
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LOCATION: (1).7.(1531)
OTHER INFORMATION: 8=9
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OTHER INFORMATION: w=a
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NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b=g
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      AME/KEY: misc_feature
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Matches 149;
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US-09-795-668-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.1%; Score 120.4; DB 10; Length 7680; 74.3%; Pred. No. 9.5e-24; ive 0; Mismatches 56; Indels 1;
                                                                                                  Sequence 3, Application US/09939581A
Patent No. US20020102245A1
GENERAL INFORMATION:
APPLICANT: Hermeking, Heiko
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
FILE REPERBNCE: 1107.77810
CURRENT APPLICATION NUMBER: US/09/939,581A
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Patent No. US20020165144A1
GENERAL INPORMATION:
APPLICANT: Stefanson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/210,748
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
481 AAGCTCTGAGGGACTGACGT 500
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LOCATION: (1)...(1531)
OTHER INFORMATION: r=g or a
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Best Local Similarity 74.3
Matches 165; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
LENGTH: 7680
                                                                                   US-09-939-581A-3
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166 CAAAAAACACTACAATTTTTGTTTTGTTTTGTTTTTGAGACAGGGTCTCGAGGTGT 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 CACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 532425 CGCCCAGGCTGGAGTGCAGTGGCGGATCTCGGCTCACTACTAGCTCCGGCCTCCGGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.0%; Score 120; DB 9; Length 1503841; 82.8%; Pred. No. 2.4e-22; ive 0; Mismatches 30; Indels 1;
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Fatent No. US20020045577A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansward
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                          ) LOCATION: (1)...(1531)
) OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1
NAME/KEY: misc feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1).7.(1531)
OTHER INFORMATION: h=a or c or t/u
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SEQ ID NOS: 1531
FastSEQ for Windows Version 4.0
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OTHER INFORMATION: n=a or g or c or t/u
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OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
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OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
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OTHER INFORMATION: s=g or c
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OTHER INFORMATION: d=a or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(1531)
OTHER INFORMATION: b=g
                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(1531)
OTHER INFORMATION: h=a
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OTHER INFORMATION: v=a
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LOCATION: (1)...(1531)
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                                                          1503841
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                                        SEQ ID NO 1
  NUMBER OF
SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 120, DB 10, Length 1503841;
Pred. No. 2.4e-22;
0; Mismatches 30; Indels 1;
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NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-668-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
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OTHER INFORMATION: h=a or c or c/u
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OTHER INFORMATION: v=a or g or NAME/KEY: misc_feature
                                                                                                                                             LOCATION: (1)...(1531)
OTHER INPORMATION: k=g or t/u
NAME/KEY: misc [eature
LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
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Best Local Similarity 82.8%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                    LOCATION: (1) ... (1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
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                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                     NAME/KEY: misc_feature LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
                                                          LENGTH: 1503841
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US-09-795-686-1
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Score 120; DB 10; Length 1503841;
Pred. No. 2.4e-22;
0; Mismatches 30; Indels 1;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO06
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application date removed - consult PALM or file wrapper
SOFTWARE: PALENTI NOS: 10231
SOFTWARE: PALENTI NE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8718, Application US/09764891; Publication No. US20030077808A1; GENERAL INFORMATION:
     24.0%;
82.8%;
     Query Match 24.0
Best Local Similarity 82.8
Matches 149; Conservative
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APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT APPLICATION NUMBER: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28

Sequence 1, Application US/09795686 Patent No. US20020094954A1

GENERAL INFORMATION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8719, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8119
; LENGTH: 4045
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                                                                                  Length 4045;
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                                                                                  DB 9;
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Pred. No. 9.9e-24;
0; Mismatches 57
                                                                                  24.0%; Score 119.8; DB 9
73.0%; Pred. No. 9.9e-24;
                                                                                                                   0; Mismatches
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US-08-927-939-78/c
; Sequence 78, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 73.0%;
Matches 154; Conservative
                                                                             Query Match
Best Local Similarity 73.0
Matches 154; Conservative
              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8718
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; ORGANISM: Homo sapiens
US-09-764-891-8719
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US-09-764-891-8719
LENGTH: 4045
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; Patent No. USCO020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc; TITLE OF INVENTION: Gene Sets
; TITLE OF INVENTION: Gene Sets
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 69220-77
; CURRENT APPLICATION NUMBER: US/60/233,133
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR FILING DATE: 2000-09-22
; PRIOR FILING DATE: 2000-09-22
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TITLE OF INVENTION: Compounds and methods to inhibit or TITLE OF INVENTION: augment an inflammatory response. FILE REFERENCE: 295.022US1 CURRENT APPLICATION NUMBER: US/08/927,939 CURRENT FILING DATE: 1997-09-11 NUMBER OF SEQ ID NOS: 83 SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 5.6e-24;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8;
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Pred. No. 5.6e-24;
0; Mismatches 29
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Best Local Similarity 82.5%;
Matches 137; Conservative (
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Best Local Similarity 82.5%;
Matches 137; Conservative
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                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-954-531-146
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; NAME/KEY: CDS
; LOCATION: (27)...(299)
US-08-927-939-78
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Best Local Similarity 77.7%;
Matches 143; Conservative
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ORGANISM: human
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                                                                                                                                                                                                                APPLICANT: MERKULOW, Gennady V. et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO1012CON
CURRENT APPLICATION NUMBER: US/10/237,859
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASLEG for Windows Version 4.0
SEQ ID NO 3
LENGTH 73467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25798 AGTGGTGCGATCTCGGCTCACTGCAAGCTCCGCGTCCCGGGGTCACGCCATTCTCCTGCCT 25739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09748127

Batent No. US20020076774A1

GENERAL INFORMATION:
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FITLE OF INVENTION:
FITLE OF INVENTION:
FILE REFERENCE:
CURRENT PAPLICATION NUMBER: US/09/748,127

CURRENT FILING DATE:
NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 17752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 AGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCGATTCTCCTGCCT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 TTTGTTTTGTTTTGTTTTTGAGACAGGGTCTCGAGGTGTCACCCCAGGCTGGAGTGC 242
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Pred. No. 9.7e-23;
0; Mismatches 27; Indels
                                                          647 GCCTCAGCCTCCGAGTAGCTGGGACTACAGGCGCCCGCTACCACG 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25738 CAGCCTCCCAAGTAGCTGGGACAACAGGCGCCCGCCACCACG 25697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature;
CCATION: (1)...(73467)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1) ... (17752)

CTHER INFORMATION: n = A,T,C or G

US-09-748-127-3
                                                                                                                                                            , Sequence 3, Application US/10237859
; Publication No. US20030022309A1
; GENERAL INFORMATION:
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23.8%;
Best Local Similarity 83.3%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                         US-10-237-859-3/c
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US-09-748-127-3
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Length 17752;

23.7%; Score 118.4; DB 10;

Query Match

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                                                                                  Db 15124 AAATT†CCTT†CTTTTTTTTTTTTTTTTTTTTTTTAGAGGGAGTCTCACTCTGTCACCC 15183
                                                                                                                                                       15184 AGGCTGGAGTGCAGTGGTGTGATCTTGGCTCACTGCAGCTCCGCCTCCGGGTTCAAGCC 15243
                                                                                                                                                                                                            15244 ATTCTCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGTGCCACCACGCCCAGC 15303
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                                                 FTGAGACAGGGTCTCGAGGTGTCACCC 230
                                                                                                                      231 AGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCG 290
                                                                                                                                                                                          291 ATTCTCCTGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCCACGTAAAAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AGAGGICAAGAICACGCAGCIAACAAAIGAGCCAAGACICTIGCIIITAGAGCIIGICCIC 147
                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 GACAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCA
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Pred. No. 5.7e-23;
0; Mismatches 41;
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                                                   171 AACACTACAATTTTTTTTTTTTTTTTT
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Db 11696 CAGGCGCCCGCCACCACGCCCAGCTAAT 11669

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TITITGITITGITITGTTTTGATTTTGAGACAGGGTCTCGAGGTGTCACCCCAGGCTGGAGT 240
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                                             Sequence 3707, Application US/09764877

Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

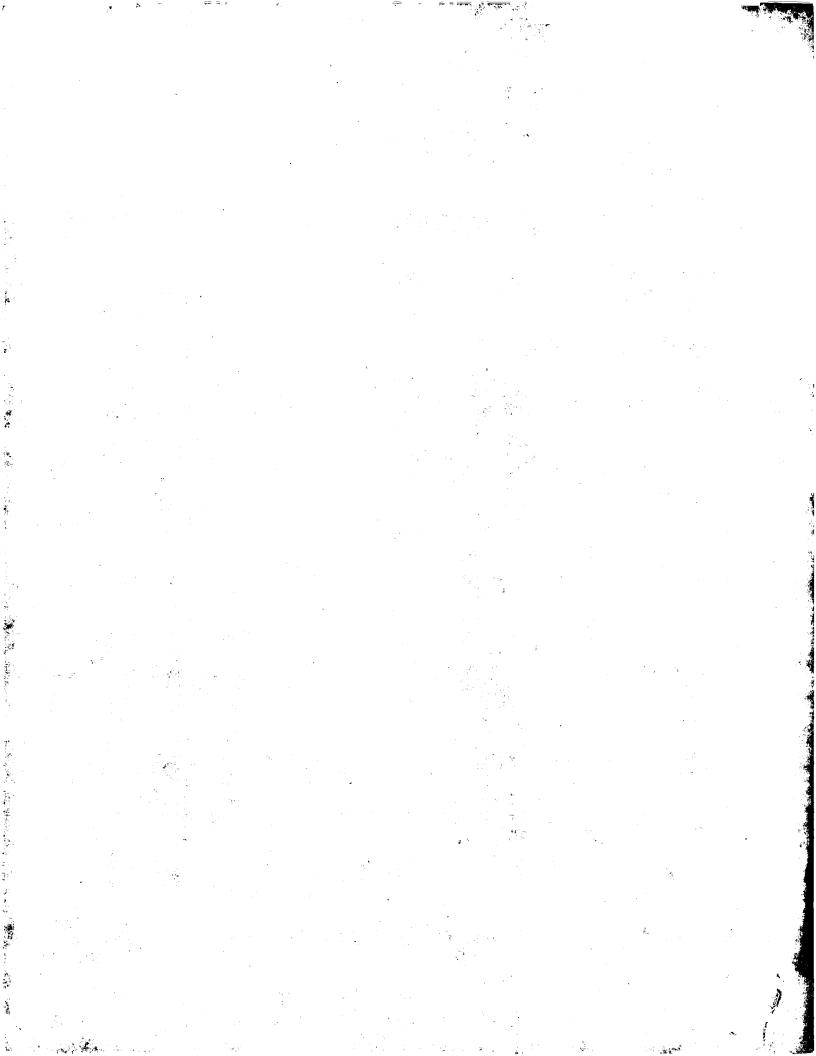
NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3707

LENTH: 5159
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; Publication No. US20030077808A1
; GENERAL INFORMATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
    FILE REFERENCE: PC006
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
    NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8002
; LENGTH: 6834
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Pred. No. 3.2e-23;
0; Mismatches 28; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.8%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-877-3707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8002
RESULT 14
US-09-764-877-3707
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US-09-764-891-8002
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Search completed: May 18, 2003, 00:34:37 Job time : 1804.39 secs



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LOCATION: (23045)..(26452)
OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23: OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation OTHER INFORMATION: signal: 26447-26452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: variation
LOCATION: (826). (23879)
OTHER INFORMATION: s at positions 826 and 23180 is G or C; y at
OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at
OTHER INFORMATION: positions 22211 and 23879 is A or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (23045)..(264
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                                                                                                                                                         May 17, 2003, 15:56:54 ; Search time 28.1345 Seconds (without alignments) 5450.193 Million cell updates/sec
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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Compugen Ltd.
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US-09-173-914-6
US-08-724-394A-21
US-08-724-394A-22
US-08-757-223-7
US-09-488-856A-10
US-09-797-906-3
US-08-759-939-5
US-08-759-835-5
US-08-759-835-5
US-08-759-835-5
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US-09-210-748A-3
US-09-851-896-3
US-09-797-906-3
US-09-732-025-3
US-09-734-673-3
US-09-851-896-3
US-08-310-356-36
PCT-US92-06300-1
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US-09-347-114A-80
US-08-975-080-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                        version :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 nucleic search, using sw model
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                        GenCore (c) 1993
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                                               Copyright
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FACERIC NO. 6333403

GRERAL INPORMATION:

APPLICANT: Tavigian, Sean V.

APPLICANT: Tavigian, Sean V.

APPLICANT: Tavigian, Sean V.

APPLICANT: Sommens, Johanna M.

APPLICANT: Sommens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Cromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/564,805

CURRENT FILING DATE: 1090-11-06

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR APPLICATION NUMBER: 09/434,382

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240
                                                                                                                                                                Sequence 3, Appli
Sequence 12, Appli
Sequence 3, Appli
Sequence 629, App
Sequence 630, App
Sequence 5, Appli
Sequence 5, Appli
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19, Appl
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6, Appli
                                                                                                                                                                                                                                                                                                                   651, App
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (910)...(13104)
OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
OTHER INFORMATION: B186-8244; exon 9: 12878-12936; exon 10:
NAME/KEY: misc feature
LOCATION: (13756)...(22917)
OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon 7: 7075-7194; exon 8: 7075-7104; exon 10: 100-7104; exon 11: 13756-13868; exon 12: 15283-15378; exon 10: 707HER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15: 707HER INFORMATION: 22172-22310; exon 18: 22879-22917
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US-09-0078-294-27
US-09-345-88-3
US-08-36-025A-19
US-08-36-048-5
US-08-965-048-6
US-09-741-154-3
US-09-741-154-3
US-09-741-156-3
US-09-741-156-3
US-09-741-156-3
US-09-741-156-3
US-09-641-638-639
US-09-641-638-630
US-09-641-638-630
US-08-641-638-631
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; Sequence 28, Application US/09564805
; Patent No. 6333403
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Query Match 23.9
Best Local Similarity 80.5
Matches 140; Conservative
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ORGANISM: Human
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LENGTH: 84495
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24.1%; Score 120.4; DB 4; Length 7680;
Best Local Similarity 74.3%; Pred. No. 8.1e-25;
Matches 165; Conservative 0; Mismatches 56; Indels 1;
                                 100.0%; Score 500; DB 4; Length 26664; 100.0%; Pred. No. 8.5e-133;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VOGELETAIN, BETT
APPLICANT: Kinzler, Kenneth
TITLE OP INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
FILE REFERENCE: 1107-77810
CURRENT APPLICATION NUMBER: US/09/210,748A
CURRENT APPLICATION NUMBER: 06/069,416
PRIOR APPLICATION NUMBER: 60/069,416
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows-Version 3.0
SEQ ID NO 3
LENGTH: 7680
                                                                     ..
0
                                                                   0; Mismatches
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Patent No. 6335156
GENERAL INFORMATION:
APPLICANT: Hermeking, Heiko
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                                                                   Matches 500; Conservative
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ORGANISM: Homo sapiens
US-09-210-748A-3
                                                 Similarity
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US-09-210-748A-3
US-09-564-805-28
                                  Query Match
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Sequence 3, Application US/09797906
Patent No. 6329188
GENERAL INFORMATION:
APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASESEQ for Windows Version 4.0
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5946 riririgingiririrgiririgagacagacirirgcicitateeeeagacidagaaga 6005
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                                                        GTGGCGCGATTTCGACTCACCGCAACCTCCGCCT-CCGCGCTTAAGCGATTCTCCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31740 CTCAGCCTCCCGAGTAGCAGGGATTACAGGAACGTGCCACCATGCTCAGCTAAT 31687
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                                                                                                                                                               303 CAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCCACG 344
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Pred. No. 3.3e-24;
0; Mismatches 34;
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Patent No. 6410325
GENERAL INFORMATION:
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LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or
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80.5%;
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ORGANISM: Human
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US-09-734-673-3
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 US-09-739-455-3
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LENGTH: 11
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APPLICANT: WEI, MING-Hui et al
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001011
CURRENT APPLICATION NUMBER: US/09/732,025
CURRENT APPLICATION NUMBER: 2000-12-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                 86 TGAGAGGTCAAGATCACGCAGCTAACAAATGAGCCAAGACTCTTGCTTTAGAGCTTGTCC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 cirrirccirciririrgaarrcrrrrrgagcaagragirigigerigigirgiriric 337
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                                                                                                                                                              146 TCTATTCTTGCTTTCCTTCCAAAAACACTACAATTTTTGTTTTGTTTTGTTTT
                                                                                                                                                                                         GAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 CTATICITIGCTTTTCTTTCCAAAAACACTACAATTTTTGTTTTTGTTTTTGTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGACAGGGTCTGGCTCTGTCACCCCAGGCTGGAGTGCAGTGGCGCAATCCAGGCTCACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCTCCGCCTCCGCGCTTAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCTCTGCCTCCCGGCTCCAGCGATCCTCCTAGCTCAGCCTCCCAAGTAGCTGGGACAA
                                                                                                                                                                                                                                                                                                CAACCTCCGCCTCC-GCGCTTAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACAGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGC
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                                    Length 84495
                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                DB 4;
                                                                  . 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.1%; Score 115.4; DB 4; Best Local Similarity 74.1%; Pred. No. 2.2e-23; Matches 146; Conservative 0; Mismatches 51;
                              Score 115.6; DB 4
Pred. No. 4.9e-23;
0; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                               16000 recaegrecececececeaecraer 16029
                                                                                                                                                                                                                                                                                                                                                                 TACAAGCTCGGGACACCACGTAAAAATGAT 354
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LOCATION: (1)...(8285)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09732025
Patent No. 6416990
                              Query Match 23.1%;
Best Local Similarity 66.7%;
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGCTCGGGACACCAC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGCTCATGTCACCAC 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
LENGTH: 8285
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-732-025-3
US-09-797-906-3
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APPLICANT: GUBGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01020
CURRENT APPLICATION NUMBER: US/09/734,673
CURRENT APPLICATION NUMBER: US/09/734,673
KURBEN OF SEQ ID NOS: 6
SOFTWARE: FASELSEQ for Windows Version 4.0
Sequence 3, Application US/09739455
Patent No. 6413756
Retent No. 6413764
APPLICANT: TANORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00653
CURRENT APPLICATION NUMBER: US/09/739,455
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4:0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2129 cirrirccircirrirgaarrcrrrrgagcaagiagirigicricrcgrigirgirig 2188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AACCTCCGCCTCCGCGCTTAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 CTTGCTTTAGAGCTTGTCCTCTATTCTTGCTTTTCTTTCCAAAAACACTACAATTTTTG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2189 AGACAGGGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGGCGCAATCCAGGCTCACGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 AGACAGGICTCGAGGIGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGC
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Best Local Similarity 67.3%; Pred. No. 5.3e-23;
Matches 177; Conservative 0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.1%; Score 115.4; DB 4 Best Local Similarity 74.1%; Pred. No. 2.6e-23; Matches 146; Conservative 0; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NOAME/KEY: misc_feature
LOCATION: (1)...(11827)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1). ... (38564)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-673-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09734673
Patent No. 6410294
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2309 CAGGCTCATGTCACCAC 2325
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ZIP: 19426
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System 7.0
SOFTWARE: Microsoft Word Version 5.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,356
  ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
                                                                                                                                                                                                                                                                                           APPLICATION: 800
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/737,853
FILING DATE: 31-UL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A0856
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3808
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
TENTYH: 19011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: intron
LOCATION: 1855..2563
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /label= intron1
OTHER INFORMATION: /citation= ([1])
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NAME/KEY: exon
LOCATION: 4076..4208
OTHER INFORMATION: /number= 3
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1737..1854
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /citation= ([1])
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LOCATION: 2564..2621
COTCATION: /number= 2
OTHER INFORMATION: /citation= ([1])
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LOCATION: 6802..6934
OTHER INFORMATION: /number= 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 19011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FBATURE:
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LOCATION: 2622..4075
OTHER INFORMATION: /number=
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OTHER INFORMATION: /number=
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LOCATION: 4209..6040
OTHER INFORMATION: /number=
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LOCATION: 6041..6252
OTHER INFORMATION: /number=
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                                                                                                  COUNTRY:
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US-09-851-896-3
US-09-851-896-3
Sequence 3, Application US/09851896
Patent No. 6410325
GENERAL INFORMATION:
PAPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
CURRENT APPLICATION UNMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                    13501 GTCTCGCTCTGTCACCCAGGCTGGAGTACAGTGACGCGATCTCGGCTTACTGCAAGCTCC 13560
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32942 GCATGATCTTGGCTCACTGCAACCTCCCGGCTTCAAGCGATTCTCCTGCCTCAG 33001
                                                                                                                                                                                                                                                                                                                 33002 CCTCCCAAGTAGCTGGGATTACAGGCATGTGCCACCATGCCTAGCTGATTTTGTGTTTTT 33061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13441 İGIGGIACİTIATAGITIACAGGATTITİTİTİTİTİTİTİTİTİTİTİTİGAĞACAĞA 13500
                                                                                                                                                                       247 GCGCGATTTCGACTCACCGCAACCTCCGCCT-CCGCGCTTAAGCGATTCTCCTGCCTCAG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 GCCTCCGCGCTT-AAGCGATTCTCCTGCCTCAGCCTCCAAGTAGCTGGGACTACAAGCT 332
                                                                                                                                                                                                                                                                  306 CCTCCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGATCAAGTTCTAAC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 TGCTTTTCTTTTCCAAAAAACACTACAATTTTTTGTTTTTGTTTTTGTTTTTGAGACAGG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 GTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 70000;
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Best Local Similarity 77.6%; Pred. No. 2.9e-22;
Matches 149; Conservative 0; Mismatches 42; Indels
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Sequence 36, Application US/08310356

Patent No. 5648243

GENERAL INFORMATION:
APPLICANT: Hurwitz, David R
APPLICANT: Nathan, Margret
APPLICANT: Shani, Moshe
TITLE OF INVENTION: Transgenic Protein Production
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         33062 AATAGAGATGAGGTTTCACCATG 33084
                                                                                                                                                                                                                                                                                                                                                             366 ATGTATGCATACGAATTACAATG 388
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ORGANISM: Homo sapiens
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LENGTH: 70000
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LOCATION: 6935...759

PRATURE:

NAME/KEY: exon

LOCATION: 7759..7866

OTHER INFORMATION: /number= 6

FATURE:

NAME/KEY: exon

LOCATION: 944..9573

OTHER INFORMATION: /number= 6

PRATURE:

NAME/KEY: intron

LOCATION: 944..9573

OTHER INFORMATION: /number= 7

FEATURE:

NAME/KEY: intron

LOCATION: 10867.11081

PRATURE:

NAME/KEY: exon

LOCATION: 10867.11081

PRATURE:

NAME/KEY: intron

LOCATION: 11082.1249

PRATURE:

NAME/KEY: intron

LOCATION: 12614.13701

PRATURE:

NAME/KEY: intron

LOCATION: 12614.13701

PRATURE:

NAME/KEY: intron

LOCATION: 13800.14976

OTHER INFORMATION: /number= 9

FRATURE:

NAME/KEY: intron

LOCATION: 13800.14976

OTHER INFORMATION: /number= 10

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LOCATION: 13514.15757

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NAME/KEY: intron

LOCATION: 1516..15533

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LOCATION: 1516..15533

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NAME/KEY: intron

LOCATION: 15780..17064

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LOCATION: 15033..17064

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OTHER INFORMATION: /number= 13

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NAME/KEY: exon

LOCATION: 15767..17764

OTHER INFORMATION: /number= 13

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NAME/KEY: exon

LOCATION: 17697..17764
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3098 GCGCAATCTCGGCTCACTGCAAACTCCGCTCCCGGGTTCACGCCATTCTCCTGCCTCAGC 3157
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                                                                                                                                                                                                                                    CCATION: 1010 (1776..1854, 2564..2621, 4076..4208, LOCATION: 6041..6252, 6802..6934, 7759..7856, 9444..9573, LOCATION: 10867..11081, 12613, 13702..13799, LOCATION: 10867..11081, 12613, 13702..13799, LOCATION: 17697..15115, 15534..15757, 16950..17082, LOCATION: 17697..17741, OTHER INFORMATION: /product= "human serum albumin" OTHER INFORMATION: /cication= ([1])
FEATURE: NAME/KEY: exon LOCATION: /location= ([1])
OTHER INFORMATION: /number= 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORS: Mindetti, P P
ORS: Ruffner, D E
ORS: Ruffner, D E
ORS: Ruffner, D E
ORS: Beatrie, W-J
ORS: Deanison, O E
ORS: Deanison, O E
ORS: Deatrie, W G
ORS: Dagaiczyk, A
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PCT-US92-06300-1
SGQUENCE 1, Application PC/TUS9206300
GENERAL INFORMATION:
APPLICANT: Hurwitz, David R
APPLICANT: Nathan, Margret
APPLICANT: Shani, Moshe
TITLE OF INVENTION: Transgenic Protein Production
NUMBER OF SEQUENCES: 1
CORRESPONDENCE S. 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer, Inc.
STREET: 500 Virginia Ave., Bldg. 3A
CITY: Ft. Washington
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19034
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; DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-310-356-36
LOCATION: 17765..18534
OTHER INFORMATION: /number= 14
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17742..18697
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NAME/KEY:

LOCATION:

1737...175

PUBLICATION:

AUTHORS:

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JOURNAL:
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NAME/KEY:
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1299 Pennsylvania Avenue, N.W
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SEQUENCE CHARACTERISTICS:
LENGTH: 2099 base pairs
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Best Local Similarity 83.6
Matches 138; Conservative
                                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                   COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
STREET: 1655
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APPLICANT: Nguyen, Thai D.
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IS REVEALED BY NUCLEOTIDE SEQUENCE WITHIN Q11-22 OF CHROMOSOME 4 : J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.3%; Score 111.6; DB 5; Length 1 Best Local Similarity 81.6%; Pred. No. 3.8e-22; Matches 129; Conservative 0; Mismatches 29; Indels
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      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: PCT/US92/06300
FILING DATE: 19920730
CLASSIFICATION: 800
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RELEVANT RESIDUES IN SEQ ID NO:
PCT-US92-06300-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Dugaiczyk, A
MOLECULAR STRUCTURE OF
                                                                                                                                                                                    CLASSITICATION: SUCH ATTOCNEY AGENT INFORMATION: NAME: GOODMAIN, ROSAINE REGISTRATION NUMBER: 52,534
REFERENCE/DOCKET NUMBER: A085
REFERENCE/DOCKET NUMBER: A085
TELECOMMUNICATION INFORMATION: TELEFAX: (215) 962-4130
TELEFAX: (215) 962-4107
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 19557 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:

ANTI-SENSE:

PUBLICATION:

AUTHORS: Minghetti, P P
AUTHORS: Kuang, W.-J.

AUTHORS: Kuang, W.-J.

AUTHORS: Hawkins, J W

AUTHORS: Beattie, W G

AUTHORS: Beattie, A
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TITLE: OF
JOURNAL:
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US-08-938-669A-5
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AUTHORS:
AUTHORS:
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TITLE: M
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Patent No. 6171857
GENERAL INFORMATION:
Patent No. 6171857
GENERAL INFORMATION:
APPLICANT: Hendrickson, Eric
TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity;
FILE REFERENCE: B0877/7017/HK
CURRENT APPLICATION NUMBER: US/09/173,914
CURRENT FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: 60/064,557
EARLIER FILING DATE: 1997-10-17
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1696 TTTTTTTTTTTTTTTTTTTTTTTTAGGGTCTCGCTCTGTCACCCAGGCTGGAGT 1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.3%; Score 111.4; DB 4;
83.6%; Pred. No. 1.8e-22;
live 0; Mismatches 26;
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SUFTWARE: FastsED for Windows Version 2.0
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
                                                                                                                                                                                                                                                                                                                                                                                                     07425-0034
                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRICAR APPLICATION DATE:
APPLICATION DATE:
FILING DATE: 28-JAN-1997
ATTORNEY PAGENT INFORMATION:
NAME: Mendelson, Blioc
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-07
TELEPHONE: 202 383-6610
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Db 148134 CCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCCACCATCACGCCCAGCTAATTATT 148193
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    Db 148014 TTAATTTTTTTTTTTTTTTTTTGGGGGGGGTCTCGCTCTGTCACCCAGGCTGGAGT 148073
                                                                               DD 148074 GCCATGCGCGATCTCGGCTCACTGCAAGCTCCGCCTCCCGCGTTCACGCCATTCTCCTG
                                                                                                                                              300 CCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGATCAAGT
                                                     241 GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCT-CCGCGCTTAAGCGGATTCTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Tanday, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN FOLDS/MS DO Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTONREY/AGERT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 111.2; DB 2;
Pred. No. 1.3e-21;
0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                Db 148194 TGTATTTTAGTAGAGGGGGTTTCATCGTGTTAA 148229
                                                                                                                                                                                                                                       360 TCTAACATGTATGCATACGAATTACAATGGAAATAA 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS MANARE: PatentIn Palac
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION: APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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not relevant
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72.7%;
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LOCATION: 1..246240
OTHER INFORMATION: /not
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COMPUTER READABLE FORM:
COMPUTER: TENTO
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COMPUTER: TENTO
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 157; Conserv
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                                                                                                                                                                                                          12298 GCAGIGGCGGGAICICGGCICACIGCAAGCICCGCCICCCGGGTICACGCCAITCTCCIG 12347
                                                                        IGTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT 240
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                          Gaps
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                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 58'
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

WEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 53.6
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576.0200
83.6%; Pred. No. 3.8e-22;
tive 0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.2%; Score 111.2; DB 2; Best Local Similarity 72.7%; Pred. No. 1.3e-21; Matches 157; Conservative 0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature

i LOCATION: 1..246240

OTHER INFRMATION: /note= "HLA-H.CONTIG"

US-08-724-3848-20
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08724394A
Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Thomas, Winston
: Tsuchihashi, Zenta
: Wolff, Roger K.
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STRANDEDNESS: not relevant
TOPOLOGY: not relevant
DLECULE TYPE: CDNA
                        Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-08-724-394A-20
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STATE: CA
COUNTRY:
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APPLICANT:
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Gaps

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Db 148014 TTAATTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCACCCAGGCTGGAGT 148073
Db 148074 GCCATGGCGCGATCTCGGCTCACTGCAAGCTCCGCCTCCCGCGTTCACGCCATTCTCCTG 148133
                                                                                                             Db 148134 CCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCCACCATCACGCCCAGCTAATTATT 148193
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                                                                               CCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGATCAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Freder, John N.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: ISM COMPATIBLE
COMPUTER: ISM COMPATIBLE
COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 53.6
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELEPONMICATION INFORMATION:
TELEPONMICATION INFORMATION:
TELEPONMICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                  Db 148194 TGTATTTTTAGTAGAGGGGGTTTCATCGTGTTAA 148229
                                                                                                                                                                                             360 TCTAACATGTATGCATACGAATTACAATGGAAATAA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
| LOCATION: 1..246240
| OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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US-08-724-394A-22
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        Qy
        241
        GCAGTGGGCGCGATTTCGACTCACCGCACTCCGCCTTAAGCGATTCTCCTG
        299

        Db
        148074
        GCCATGGCGCATCTCGGCTCACTGCAGCTCCGCGCTTCACGCCATTCTCCTG
        148133

        Qy
        300
        CCTCAGCCTCCCAGGACTACAGCTCGGGACACCACGTAAAAATGATCAAGT
        359

        Db
        148134
        CCTCAGCTCCCGAGTAGCTGGAACTACAGGCCCACCATCACGCCCAGCTAAATTTT
        148193

        Qy
        360
        TCTAACATGATAGAATGAAATGAAATGAAATAAAAA
        395

        Db
        148194
        TCTAACATTTTAGTAGAATTCAATCGTGTTAA
        148229
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Search completed: May 17, 2003, 16:46:58 Job time : 416.134 secs

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GenCore version 5.1.5
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May 17, 2003, 15:56:54; Search time 2075.34 Seconds (without alignments) 11232.524 Million cell updates/sec 1 agtgcctgtcctggtatttt......agcggaagctttgaccggat 801 4109280 2054640 segs, 14551402878 residues Total number of hits satisfying chosen parameters: US-09-434-382-28_COPY_21800_22600 801 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 gb ba: *
gb by: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		AC005277 Homo	1S2 AF304369 HOMO 6	AKU94012 HOMO B	ANO.14244 DOMO B	ANUGASS HOMO	AFSUGBOW GOLLI	0 AF304370	מאיטון כשכוויים איניטטאיני	ANDERSE BOMES	S AA403623 Seque	BCOOLSSY ACHOO	DCCC4158 ACM	ANOVAGG / DOMO /	1 AC128351 KALLU 57 AC128351 KALLU	75.145 145	1 AC097911 Ratti	96 AF308696 Mus	.5 AF429315 Homo	.2 AC013762 Homo	3 AC019123 Homo	AC026782 Homo	AC002364	ACC25007 MOIIIO	AC130575 Ratt	AC127320	1 AC009501	.4 AC068044	AP004782	AL359852	4 AC026114	1 ACU20611	25024 AD004	AP004303 Orv	AF063866 Me	4 AC011154 Home	.8 АРООЗ968 НОШС	.3 AC096713 Homo	AC019005 Hom	P4 AL0354 // PIAS	JUBI ALGESTURI MOL	321 AC125321 MUS	orentary orongerous	ALIGNMENTS		88 bp DNA linear	, clone hRPK.597 M 12, complete sequenc				Craniata; Vertebrata; E	Catarrhini; Hominidae; Homo	
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Complement (16474. . 16544)

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complement (5963. .6275)
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                                                               complement (4896. .5186)
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9662. .9829
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5219. .5479
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                                                                                                                                  family="L2"
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                                                                                                                                                                                                                                                                                                                                                                  L. Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.

Barearch, 320 Charles Street, Cambridge, MA 02141, USA.

Barren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Barren, S., Barna, N., Beckerly, R., Genen, J., Boatin, C., Bouvon, K., Dewar, K., Done, I., Etemadi, S., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Garge, D., Gardyna, S., Gensheimer, S., Geraglery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J. C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meltim, J., Mohla, M., Morris, W., Mortow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Nioff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Rop, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 23, 1998 this sequence version replaced gi:3335015. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Only the first 118.8 kilobases of this clone are being submitted. The remainder overlaps accession number AC005274 (WICGR project L350).
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Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 740)

Tavtigian, S. V., Simard, J. Teng, D.H.F., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Lablanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S. C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., and Cannon-Albright, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Davtigian, S.V., Carillo, A.R., Chen, Y., Bayananth, P., Desrochers, M., Dumont, M., Farnk, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Ilev, D., Janeck, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B. Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J.
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Homo sapiens putative prostate cancer susceptibility protein HPCZ/ELAC2 gene, exon 17 and partial cds.
                                                                     GCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTTT
                                                                                                                                CCAAACTTGCCCAGAGCTTTTGTTACTCATCTCTGGCTAGGAAATGGTTTTTTTGCAAAAC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 800.6; DB 9 99.9%; Pred. No. 1.3e-196; Live 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                             note="Single-stranded coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="(GGGAA)n"
complement (26576. .26781)
/rpt_family="MBR6B"
complement (26912. .26990)
/rpt_family="MBR2iB"
26991. .27290
                                                                                                                                                                                                                                                                                                                           complement (25994. .2609)
/rpt family="purine-rich"
complement (26122. .26291)
/rpt family="MLTID"
26312. .26337
                                     /rpt_family="LiM4"
21799. .22104
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'5816. .25895
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28034. 28107
family="AluSx"
ement(2)
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...26480
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complement(27291. .
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/rpt_family="LTR28"
28920..29005
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                                                                                                       rpt_family="AluJo"
2151. .22562
                                                                                                                                                                                       'rpt_family="AluSq'
:485<u>2</u>. .25199
                                                                                                                                               rpt family="MSTA" 3978. .24287
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29140. .29233
                                                                                                                                                                                                                             /rpt_family="L2"
complement(25697.
        complement (21101
                                                                                                                                                                  .24287
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Conservative
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                                                                                                ACCESSION
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AUTHORS
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                                     prostate cancer susceptibility
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Pred. No. 4.1e-178;
1; Mismatches 0;
                                                                                       /product="putative prostate
HPC2/ELAC2"
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                                                                                                             protein id="AAG24440.1"
db xref="GI:10880931"
             /product="putative p
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chromosome="17"
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/codon_start=2
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ilarity 99.9%;
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(Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (B-mall:genomics@hri.co.jp, Tel:81-438-52-9975, Fax:81-438-52-3986) NBOb human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Hell:Research Institute (HRI) (supported by Japan (Rey Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
Homo sapiens CDNA FLJ36693 fis, clone UTERUZ008901, highly similar to Homo sapiens putative prostate cancer susceptibility protein HPCZ/ELAC2 mRNA.
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Isogai, T., and Yamamoto, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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to mRNA, clone_lib:UTERU2
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/tissue type="ulbarus"
/clone lib="UTBRU2"
/note="cloning vector: pME18SFL3"
/note="cloning vector: pAF18SFL3"
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/db_xref="taxon:9606"
/clone="UTERU2008901"
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ilarity 89.1%;
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Matches 156; Conserv
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Direct Submission

Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome (Enter; Shirokame-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ins.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
                                                                                                                                                                                                                                                                                                                                                                                                                                           oligo capping; fis (full insert sequence). Home sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nokancto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO, human cDNA sequencing project
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Pred. No. 6.3e-27,
1; Mismatches 18
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/db_xref="taxcn:9606"
/clone=HEP03495"
/cell_ine="HepG2"
/cell_type="hepatoma"
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/clone_lib="HBP"
/note="cloning vecto:
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Best Local Similarity 89.1%;
Matches 156; Conservative
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Homo sapiens
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Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA ilbrary construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5-6, and one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and
                                                                                                                                                                                                          AK094333 2734 bp mRNA linear PRI 15-JUL-2002
Homo sapiens cDNA FLJ37014 fis, clone BRACE2010203, highly similar
Lo. Homo sapiens prostate cancer susceptibility protein HPC2/ELAC2
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Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamachita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Yakahsahi-Eujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                          AK004333.1 GI:21753374
oligo capping; fis (full insert sequence).
Homo sapiens cerebellum cDNA to mRNA, clone_lib:BRACE2
845 CTGGGCACCTGGCTGCTGTGTTTTGTGTCCCACCTGCACGAGATCACCACGG
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Pred. No. 6.4e-27;
1; Mismatches 18;
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/clone_lib="BRACE2"
/note="cloning vector: pM
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/clone="BRACE2010203"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAG24916.1"
/db_xref="G1:10946489"
/translaterPRKDPLRHLRTRE
KRGSGGGGFOTTVYVAGSRDSGAALTVFSEFNRYLFNCGEGVQRLMQEHKLKV
KRGPSGCGGFOTTVYVAGSRDSGAALTVFSEFNRYLFNCGEGVQRLMQEHKLKV
VRLDNIFLTRHWWSVVGGLSGNILTLKETGLFKCVLSGSPQLERYLBAIKIFSGPLKG
IELAVRPHSAPEYEDETMTVYQIPIHSEQRRGRHQPWQSPERPLSRLSPERSSDSESN
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APVLOKUSTHFGKEILAELCTPPDGAAFVUVGCPBEST 10PT CEMTYFGRYGKAD
APVALVYHMAPESVLVUDSRYQQMMERFGPDTQHLVLNENCASVHNLSGHKIGTCLNLI
HPDIFPLLTSPPCKKEGPTLSVPMVGGECLLKYQLRPRREWGRDAIITCNPEEFIVEA
LQLPRPQSVGORRRSVODVPAPAERKSGYPEITFGTGSCAFINKISTWSATLVNISP
LOTSLLLDCGEGTFGQLCRHYGDOVDRVLGTLAAVFVBHLADHHTGLINILLOKEQAL
ASLGKPLHPLLVVAPSQLKAMLQQYHNGCOBVLHHISMIPAKCLQEGAEISSPAVERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84103, USA
          PRI 27-FEB-2001
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Taviignan, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K.E., Beaterson, K.T., Reld, J.B., Richards, S., Schroeder, M., Penn, B., Swder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., and Cannon-Albright, L.A. Skolnick, M.H., Neuhausen, S., Rommens, J. Gorilla gorilla ortholog of human HPC2/ELAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="similar to Homo sapiens HPC2/ELAC2"
AF308694 2893 bp mRNA linear
Gorilla gorilla ELAC2 (ELAC2) mRNA, complete cds.
AF308694
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/organism="Gorilla gorilla"
/db_xref="taxon:9593"
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                                                                          AF308694.1 GI:10946488
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                                                                                                                   Gorilla gorilla.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 2908)

Tavtigian,S.V., Simard,J., Teng,D.H.F., Abtin,V., Baumgard,M.,
Beck,A., Camp,N.J., Carillo,A.R., Chen, Frank,D., Frye,C.,
Ghaffari,S., Gupte,J.S., Hu,R., Iliev,D., Janecki,T., Kort,E.N.,
Laity,K.E., Leavitt,A., Lebland,G., McArthur-Morrison,J.,
Pedreson,A., Penn,B., Peterson,K.T., Reid,J.E., Richards,S.,
Schroeder,M., Smith,R., Snyder,S.C., Swedlund,B., Swensen,J.,
Thomas,A., Tranchant,M., Woodland,A.M., Labrie,F., Skolnick,M.H.,
Neuhausen,S., Rommens,J. and Cannon-Albright,L.A.
A candidate prostate cancer susceptibility gene at chromosome 17p
ISSLIRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTWPCEALVRMGKDATL
LIHBATLEDGLEEBAVEKTHSTTSQALSVGWRMNAEFIMLNHFSQRYAKVPLESPNFN
EKVGVAFDHWKVCFGDFPTWPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSGE
LAGGLEDGEPQQRAHTEEPQKKVRAQ"
1787 c 815 g 586 t
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Tavtigian, S. V., Simard, J., Teng, D. H. F., Baumgard, M., Beck, A., Gamp, N. J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J. M., Frank, D., Frye, C., Ghaffari, S., Gupte, J. S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K. E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, K. T., Reid, J. E., Richards, S., Schroeder, M., Smith, R., Snyder, S. C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A. M., Labrie, F., Skolnick, M. H., Neuhausen, S., Rommens, J. and Cannon-Albright, L. A.
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/product="putative prostate cancer susceptibility protein
HPC2/ELAC2"
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                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 6.4e-27;
1; Mismatches 18;
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/db_xref="taxon:9606"
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Best Local Similarity 89.1%;
Matches 156; Conservative
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Similarity
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Matches 156;
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RS Tavtigian, S. V. Simard, J. Teng, D. H.F., Abtin, V. Baumgard, M., Beck, A., Camp, N.J., Teng, D. H.F., Abtin, V. Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Franham, J. M., Frank, D., Frye, C., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E. Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pedarson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
A candidate prostate cancer susceptibility gene at chromosome 17p E 21096277
                                         / translation="MWALCSLLRSAAGRTMSQGRTISQAPARRERPRKDPLRHLRTRE
KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVPSEFNRYLFNCGEGVQRLMQEHKLKV
ARLDNIFLTRHWSNVGGLSGMILTLKETGLRFCVLSGPPQLEKYLENIK IFSGFLKG
IELAVRPHSAPEYEDETWYVQIPILEBGRRGKHQPWQSPRRLSRLSPERSSSESN
ENEPHLPHGYSQPRRUSSLVVAFICKLHLKRGNFVLKAKEMGLPVGTAALAPIIA
AVKDGKSITHEGREILAEELCTPPDPGAAFVVVECPDESFIQPICENATFQRYQGKAD
APVALVVHMAPASVILVDSRYQQWMERFGPDTQHLVLNENCASVHNLRSHKIGTQLNLI
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LQDPWQQSVQBYRRSAQDGPRABEKRSQYPEIIFIGFGSAIPKAIRWVSATLVNISP
DTSLLLDCGEGTFGQLRHVGDOVDRVLGTLAAVFVBHLHADHFTGLSILLQRERAL
ASLGKPLHPLLVVAPNQLKAMLQQYHNQCQEVLHHISMIPAKCLQGGAEISSPAVERL
                                                                                                                                                                                                                                                                                                                                     ISSLLRTCDLEEFQTCLVRHCKÄÄFGCÄLVHTSGWKVVYSGDTMPCEALVRMGKDATL
LIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAKVPLFSPNFS
EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRGVRAALLSRE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes ELAC2 mRNA, complete cds.
AF308698
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Jacases 1 to 2908)

Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu.R., Iliev, D., Janecki, T., Kort, E.N., Laity, K., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Schroeder, M., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
Direct Submission

Direct Submission

Location/Qualifiers
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LQLPNFQQSVQEYRRSAQDGPAPAEKRSQYPEIIFLGTGSAIPMKIRNVSATLVNISP
DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLLNILLQRERAL
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ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATL
LIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAKVPLFSPNFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein id="AAG24920.1"
/db xref="G1:10946497"
/translation="MWALCSLLRSAAGRTMSQGRTISQAPARRERPRKDPLRHLRTRE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
clone lib:NT2RP2 clone:NT2RP2000985.
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Homo sapiens cDNA FLJ10530 fis, clone NT2RP2000985.
AK001392
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/db xref="taxon:9598"
1. 2481
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ilarity 89.1%;
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Homo sapiens
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NEDO human cDNA sequencing project
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Pred. No. 6.4e-27;
1; Mismatches 18
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Best Local Similarity 89.1%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (29-JAN-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC 1679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTGGCAGTGACTCTCTCTCTCTCTCTCTCAGCCCCGACACGTCTCTGCTACTGGAC 397
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                                                                                                                                                                                                                                                                                                                                                                                                             Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Xue, A.J., Yang, Y., Wehrman, T. and Drmanac, R.T. Novel nucleic acids and polypeptides
Patent: WO 0222660-A 240 21-MAR-2002;
HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGGCACCCTGGCTGCTGTTTTGTGTCCCACCTGCACGCAGATCACCACACGG 1734
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9
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89.1%; Pred. No. 6.4e-27;
iive 1; Mismatches 18
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/db_xref="taxon:9606"
75._.2555
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1. .2992
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GI:21439089
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Homo sapiens
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1666 CTGGGCACCCTGGCTGCTGTTTGTGTCCCACCTGCACGCAGATCACCACACGG 1720

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: c Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / LTAIN LALL ON THE WAALCSLLRSAACRTMSQCRTISQAPARRERPRKDPLRHLRTRE KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVPSEFNRYLFNCGEGVQRLMQBHKLKV ARLDNIFLTRNHWSNVGGLSGMILTLKETGLPRCVISGPPGLEKYLEALAKIFSGPELKG IELAVRPHSAPEYEDENSYQIPILTLKETGLPRCKHQPWQSPERPLSRESPERSSELN ENERPHLPHGYSQRRGYRDSSILVVAFICKLHLKRGNFUYLKAKEMGLPVGTAALAPIIA AVKDGKSITHEGREILAEELCTPPDPGAAFVVVECPDESFIQPICENATFQRYQGKAD
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/protein_id="AAH04158.1"
/db_xref="GI:13278771"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APVALVVHMAPASVLVDSRYQQWMERFGPDTQHLVLNENCASVHNLRSHKÏQTĞLNLI HDDIFPLLTSFRCKKEGPTLSVPMYQGECLLKYQLRRREWADRALITCNPEBETYBA LQIPDIFPLGFRXAQOSYQEYASAQOSOFABEKSQYPEIIFLGTGSAIPMKIRNVSATLINNISP DISLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
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ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATL
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                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (01-MPAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                   BC004158 3006 bp mRNA linear PRI 12-JUL
Homo sapiens, putative prostate cancer susceptibility protein,
clone MGC:2441 IMAGE:2820640, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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'clone lib="NIH MGC 7"
'lab_host="DH10B-R"
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/organism="Homo sapiens"
/db_xref="LocusID:60528"
/db_xref="taxon:9606"
/clone="MGC:2441 IMAGE:2820640"
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                                                                                                                                                                                                                                                                          BC004158.1 GI:13278770
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ORGANISM
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ORIGIN
                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                           RESULT 12
BC004158
LOCUS
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AUTHORS
                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
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COMMENT
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DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
ASLGKPLHPLLVVAPNOLKAWLQQYHQCQEVLHHISMIPACHACKGLQEGAEISSPAVBRL
ISSLLRTCDLEBEYGTCLVRHYCKHAFQACALVHTSGWKYYSGDTMPCCALVRMGKDATL
LIHBATLEDGLEBEYGTCLVRHYSTYGALSVGRRNNABEFIMLNHFSQRYAKVPLESPBNFS
EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMBERREKRELRQVRAALLSRE
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product=="putative prostate cancer susceptibility protein"
protein_id="AAH01939.1"
/db_xref="GI:LS804973"
                                                                                                                                                                                                                                                                                                                            info@bcgsc.bc.c.

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Sess, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: i Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621. Location/Qualifiers
1. .2997
Jene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1546 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGGACACGTCTCTGCTACTGGAC 1605
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                                                                                                                                                                                                            cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
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/clone lib="NIH MGC 7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteat: MGC halp desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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/db_xref="LocusID:60528"
/db_xref="taxon:9606"
/clone="MGC:4102 IMAGE:2820640"
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Pred. No. 6.4e-27;
1; Mismatches 18
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806 c 853 q 598 t
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); CDNA library
construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AK094687

Homo sapiens cDNA FLJ37368 fis, clone BRAMY2024530, highly similar to Homo sapiens prostate cancer susceptibility protein HPC2/ELAC2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       1615 TGTGGTGAGGGCACGTTTGGGCCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC 1674
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                                                                                                                        1555 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1614
                                                                          338 AGTGGCAGTGACTCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                           398 TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC 457
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Homo sapiens amygdala cDNA to mRNA, clone_lib:BRAMY2
clone:BRAMY2024530.
Homo sapiens
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  89.1%; Pred. No. 6.4e-27; ive 1; Mismatches 18;
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88.6%; Pred. No. 1.7e-26;
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/clone lib="BRAMY2"
/note="cloning vector: p
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clone="BRAMY2024530"
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AK094687.1 GI:21753794
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To (Dases 1 to 167336)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrocks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaroks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarok, J., Benton, J., Burkett, C., Burch, P. Burkett, C., Burch, B. Brown, M., Bryant, D., Bouck, J., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Coyler, Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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1547 TGTGGTGAGGGCACGTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACACGGGTC 1606
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Direct Submission
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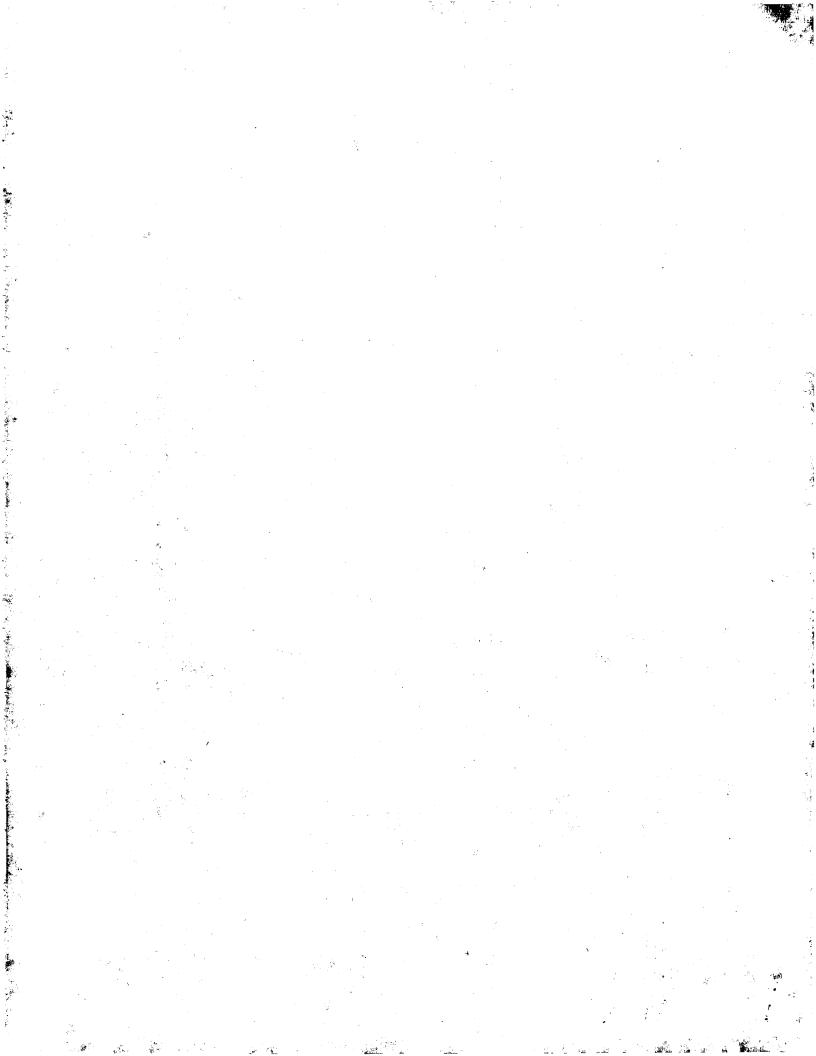
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CHVIAAPENULDSKYQWMERFGPTOYDLILLMENESKHYGYGLAIAPDI
PPQLTSFYSKEEGSTLSVPYMEGECLLKYQLRPKEWGRDTTLDCNTDEFIABLELD
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ELDCGEGTFGCOLCRHYGOLDRVLCSLTAVEVVBLHADHTGLLNILLDGRHALASLG
KPPQLLVNAPTQLRAWLQOYNHYCOEILHHYSMIPAKCLOKGAEVSNTTLEELISLIL
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LETCDLEFFCOTCLVRHYCKHAFGCALVHSSGWKVVYSGOTMFCEALVOMGKDATLLHE
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16609 ..1667,1746 ..16818,17370 ..17482,18671 ..18766,
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Search completed: May 17, 2003, 21:44:52 Job time : 2253.34 secs



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May 17, 2003, 15:56:54; Search time 1295.47 Seconds (without alignments) 11232.524 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred.

AC005277 118788 bp DNA linear PRI 23-JUL-1998 Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence. AC005277 Homo sapiens.

Homo sapiens

Eukaryotas Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryotas Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 118788)

Elsren, B., Fasman, K., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone hRPK.597_M_12

Unpublished AC023591 Homo sapi AC017038 Homo sapi AC060764 Homo sapi Continuation (3 of Homo sapi Human DNA Human DNA Homo sapi Human chr Homo sapi Homo sapi Human DNA Homo sapi Homo sapi Papio cyn Human DNA Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Human DNA score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Ношо Homo Номо Ношо Ношо Homo Homo Ношо Ношо Homo Homo Ношо Ношо Description AL355840 BAC010366 BAC022129 BAL589762 BAL121767 BAL1217 AC073228 1 AC090088 1 AC069106 AC022539 AC021718 AC091772 | AC068015 | AC116934 | AL499582 | AC111187 | AC084264 | AC022448 | AC109993 | AL645722 | AL354953 | AC022819 | AC018738 | AC074185 | AP000753 AC090382 AC015576 AC012028 AL354720 AC018999 ALIGNMENTS SUMMARIES AC060764 AC009771_2 AC012386_0 HSA524G17 AP001591 AC068015 AC018999 AC022819 AC005277.1 GI:3337311 DB Query Match Length 191468 184338 110000 110000 153185 178653 65612 178980 175642 181532 59915 24.9 24.8 24.8 24.8 24.8 124.6 124.2 124.2 124.2 124.2 124.2 124.2 123.4 123.2 123.2 123.2 123.2 123.2 123.2 Score 123.6 RESULT 1 AC005277 LOCUS DEFINITION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION Result Š. No. is the number of results predicted by chance to have a

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AL Submission

AL Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CES 3 (bases 1 to 11878)

Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Baron, A., Castle, A., Cerny, G., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Trizhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gersderry, K., Glimartin, T., Grantic, C., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Mahf, R., Nahf, R., Naylor, J., Miloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Stone, C., Strange-Thomann, A., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Stone, C., Shyam, R., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Shyam, R., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Coly, M., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and D. Suby, M.
           Libran, B., Tasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Barker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Brown, A., Castle, A., Cerrly, J., Cooke, P., Depayre, E., Boutwell, C., Brown, A., Castle, A., Cerrly, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meltin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachers, D., Rossello, R., Roy, A., Stange-Thomann, N., Stlwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 23, 1998 this sequence version replaced gi:335015. All repeats were identified using RepeatMasker: Smit, A.F.A. &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Only the first 118.8 kilobases of this clone are being submitted. The remainder overlaps accession number AC005274 (WICGR project L350).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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195. .884
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7.18. .347
/rpt_family="L2"
complement(3478. .3821)
/rpt_family="MLTIA1"
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complement(4328. .4608)
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237. .2713
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.15620)

family="(CA)n"

family="LIME3A"

family="(CA)n" ement(12=")

.19065

family="L2"

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Homo sapiens chromosome 15 clone RP11-321G12, WORKING DRAFT SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157159)
Waterston, R.H.
                        * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigg are represented as * Trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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On Jul 7, 2000 this sequence version replaced gi:7523953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-primer ET; 86% of reads Chemistry: Dye-primer ET; 86% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 148266 bases at least Q40 consensus quality: 151490 bases at least Q30 Consensus quality: 153444 bases at least Q20 Insert size: 165000; agarose-fp Insert size: 16500; agarose-fp Quality coverage: 4.15 in Q20 bases; sum-of-contigs Quality coverage: 4.15 in Q20 bases; sum-of-contigs
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unknown length
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unknown length
of 4742 bp in length
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of 5346 bp in l
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of 7084 1
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Homo sapiens
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Waterston, R.H.
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100.0%; Pred. No. 1.1e-116;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                               note="Single-stranded coverage.
                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="MERGB"
complement(26912..26990)
/rpt_family="MER21B"
26991..27290
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/rpt_family="LTR28"
28266. 28107
                                                                                                                                                                                                                                                                            complement (25994. .26099)
/rpt family="purine-rich"
complement (26122. .26291)
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complement(25697. .25985)
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complement(21348, 2):frr
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22151. .22562
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28266. .28795
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complement(27291. ..
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Matches 500; Conservative
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Stranses 1 to 15/59/0, Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Calamopolano, A., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Daz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Daz, J.S., Gardypoland, S., Garder, D., Calagan, J., Gardyna, S., Galegra, A., Horton, L., Hulme, W., Gage, D., Galagan, J., Hagos, B., Heaford, A., Horton, L., Hulme, W., Lilev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, W., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Marthews, C., McCarthy, M., McEwan, P., McKernan, K., Mrighy, T., Naylor, J., Norman, C., Norman, C., Norman, C., Norman, C., Norman, C., Norman, C., Reback, M., Rilsey, R., Rise, C., Rogov, P., Roman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Triglio, J., Vassiliev, H., Viel, R., Vo, A., Sanner, A., and Zody, M., Sannou, J., Valann, J., Nalann, J., Nalann, J., Nalann, J., L., Zinmer, A., and Zody, M.
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                                                                                                                                                                                                                     AC087525 157590 bp DNA linear PRI 14-MAY-2002
Homo sapiens chromosome 15, clone RP11-321G12, complete sequence.
AC087525
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157590)
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                                                               Db 147933 GAGTAGCTGGGACTACAGATGCCCGCCACCACCAACTAAT 147975
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312 AAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGAT 354
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/db xref="taxon:9606"
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Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Changalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gorde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, W., Indone, R., Landzares, R., Landcars, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLenn, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Matthews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schugback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talams, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Young, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC"
complement(177. .301)
/rpt family="L3"
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/note="<30 qual SNGL region"
complement (599. .940)
/rpt_family="L3"
676. .681
/note="<30 qual SNGL region"
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'note="single clone coverage"
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/rpt_family="AluJb"
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[156. .1179
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195. 1228
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.275. .1283
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343. .1349
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db_xref="taxon:9606"
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238. .1245
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/rpt_family="(A)n"
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Db 116995 GAAAAAATATTTGAGACTCCCAAGACCAGCAGGAGTTATTATACAGAATATATAAGAA 116936
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                                                                                                                                                                                                                                                                                                                                                                                                                 family="AluSg"
ement(17000
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4372. .14400
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complement(12615. .12899)
rpt_family="Aluy"
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omplement(10284. .10408)
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complement(14985, .15197)
             rpt_family="FLAM_C"
598. .8741
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4891. .14984
rpt_family="AT_rich"
omplement(50707.518
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918. .9153
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family="MER46B"
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                                                                                                                                                                                                 Db 116815 TTTGTTTTGTTTTGAGACAGAGTCTCACTCTGTTGCCCAGGCTGGAGTGCAGTGGCACGA 116756
                                                                                                                                                                                                                                                                                                      Db 116755 TCTCGGCTCACTGCAACCTCCGCCTCCTGGGTTAAAGTGATTCTCCTGGCTCAGCCTCCC 116696
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 171418)

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                                                              253 TTTCGACTCACCGCAACCTCCGCCTCC-GCGCTTAAGCGATTCTCCTGCCTCAGCCTCCC 311
133 TTAGAGCTTGTCCTCTATTCTTGCTTTTCTTTCCAAAAAAACACTACAATTTTTGTTTTGT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC023591 171418 bp DNA linear H
Homo sapiens chromosome 15 clone RP11-768L13 map 15,
IN PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 116695 GAGTAGCTGGGACTACAGATGCCCGCCACCACGCCCAACTAAT 116653
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Homo sapiens chromosome 15, clone RP11-768L13
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                   312 AAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGAT 354
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Zody, M.
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AUTHORS
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Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Stones, D., Young, G., Zainoun, J., Submitted (18 AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 20, 2002 this sequence version replaced gi:15291064.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 GAATICTATATICTGAAGTAGGAGATACTGTTATTGCTGTTATTACATTTTACACATAAG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are represented as runs of N. The order of the pieces are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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Pred. No. 4.2e-23;
0; Mismatches 125; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21023 21122: gap of 100 bp 21123 171418: contig of 150296 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-768L13"
/clone lib="RPCI-11 Human Male BAC"
39250 c 39907 g 46239 t 100 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 112692 GAGTAGCTGGGACTACAGATGCCGCCACCACCCAACTAAT 112734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: L6849
Center clone name: 768_L_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
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us-09-434-382-28_copy_1_500.rge

REFERENCE AUTHORS TITLE

ACCESSION

RESULT 5 AC017038

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Gaps
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si gap of unknown length
contig of 6723 bp in length
contig of 7719 bp in length
contig of 7719 bp in length
gap of unknown length
contig of 7699 bp in length
gap of unknown length
contig of 8859 bp in length
gap of unknown length
contig of 11813 bp in length
gap of unknown length
contig of 11813 bp in length
contig of 14814 bp in length
gap of unknown length
contig of 14814 bp in length
gap of unknown length
contig of 16327 bp in length
contig of unknown length
contig of unknown length
gap of unknown length
contig of 1834 bp in length
contig of 1837 bp in length
gap of unknown length
contig of 18671 bp in length
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Pred. No. 1.7e-22;
0; Mismatches 99;
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note="assembly_name:Contig14"
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note="assembly_name:Contig20"
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note="assembly_name:Contig12"
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note="assembly_name:Contig13"
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note="assembly_name:Contig16"
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note="assembly_name:Contig21"
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note="assembly_name:Contig23"
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note="assembly_name:Contig10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_name:Contig15"
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21943. .141936
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142037. .180707
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'note="assembly_name:Contig9"
                                                                                                                                                                                                                                                                                                                                                                                                                           ....2076
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                                                                                                                                                                                                                                                                                                                                        1. .180707
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         clone="RP11-313B2"
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105516. .121842
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Best Local Similarity 65.5
Matches 188; Conservative
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ORIGIN
                                                                                                                                                                                                                                                                                                                     FEATURES
                  ACUL/U38
180707 bp DNA linear HTG 07-JUL-2000
Homo sapiens chromosome 8 clone RP11-313B2, WORKING DRAFT SEQUENCE,
20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                        Louis,
                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 180707) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7230978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; $
Chemistry: Dye-primer ET; $ of reads
Chemistry: Dye-terminator Big Dye; $ of reads
Chemistry: Dye-terminator Big Dye; $ of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 168786 bases at least Q40
Consensus quality: 17486 bases at least Q20
Consensus quality: 17496 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 200000; agarose-fp
Insert size: 348 in Q20 bases; agarose-fp
Quality coverage: 3.86 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center
Center code: WUGSC
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                                                                                                                                                                                                                                           The sequence of Homo sapiens clone Unpublished
                                                                                                  ACO17038.6 GI.8568131
HTG; HTGS PHASE1; HTGS_DRAFT.
HOMO sapiens.
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Direct Submission
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KEYWORDS
SOURCE
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                                                   DEFINITION
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Direct Submission

Noticed (106-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

(E 4 (bases 1 to 184338)

Birran, M. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, M., Bastien, V., Lander, E., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faros, S., Fitzgerald, M., Gage, D., Galagan, J., Gardam, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lander, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Menthews, C., Norman, C., Nacon, Murphy, T., Maylor, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Norbu, C., Norman, C., Phunkhang, P., Peirre, M., Raymon, C., Raymon, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Resfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Wilson, B., Whu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Nill repeats were identified using RepeatMasker:

Smit, A. F. A. & Green, P. (1996-1997)

Http://ftp.genome.washington.edu/RM/RepeatMasker:

Smit, A. F. A. & Green, P. (1996-1997)
O'Connor, T., O Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Royan, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zimler, A. wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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1947. .1951
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complement(157. 417)
/rpt_family="LiMA9"
complement(566. 760)
/rpt_family="LiMC5"
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Center clone name: 626_A_5
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/db_xref="taxon:9606"
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1391. .1480
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1481. .1794
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complement(937...
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1. (Dases 1 to 184338)

Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-626A5
                                                                                                                                                                                                                                                                                                         Db 174368 CAGAGTCTCGCTCTGTCACCCCAGGCTGGAGTGCAATGGCAATGATCTCAGTCTCACTGCAAG 174427
                                                                       Db 174248 ATGTGACTATCAGTTAAACAATAAGAAAGTTATTTCACATTATTTGTAGTATGTCCAAAA 174307
                                                                                                                                                                                                    Db 174428 TTCCGCCTCCCGGGTTCTGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAG 174487
                                                                                                                                                                                                                                                                                                                                                                                                     270 CTCCGCCTCCGCGCTTAAGCGATTCTCCTGCCTCCAGCCTCCCAAGTAGCTGGGACTACAA 329
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Homo sapiens chromosome 8, clone RP11-626A5, complete sequence.
ACO60764
      90 AGGICAAGAICACGCAGCIAACAAAIGAGCCAAGACICITGCTIIAGAGCIIGICCICIA 149
                                                                                                                                                                                                                                                                    CAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGCATTTCGACTCACCGCAAC
                                                                                                                                       Db 174488 GCACCTGCCACACCCAGCTAATTTTTTTTGTATATTTTTAGTA 174534
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complement (3971. .3976)
/note="<30 qual SNGL region"
complement (4059. .4063)
complement (4122. .4128)
/note="<30 qual SNGL region"
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                          /ip___amily=_amily=
complement(2854.3158)
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complement(3899.3904)
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complement(3934.4089)
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complement(3911.3976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt family="Alusc"
complement (10091. .10117)
/rpt family="MRR96B"
complement (10146. .10355)
/rpt family="Aluy"
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omplement(12855, .13021)
rpt_family="MIR"
3047, .1346
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omplement(10745, .10865)
rpt_family="L2"
1163, .11304
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omplement(11343, .11622)
rpt family="AluJb"
1623, .11768
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omplement(12233, 12526)
rpt family="MER110"
2580. 12707
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13881. .14073
/rpt_family="L1MB4"
complement(14074. .14373)
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6936. 7241
/rpt_family="AluSq"
complement(8712. .8915)
/rpt_family="MIR"
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/rpt_family="MLT1B"
complement(9680 .9801)
/rpt_family="MER96B"
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791. .693E
family="AluY"
ement(?or.
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complement (5011. .5494)
rpt family="MLT1L"
complement (5802. .5971)
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| 13804. .13854
| rpt_family="LIMB3"
| 1073
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3467. .13770
                                                                                                                                                                                                                                                                                                                                                                                                  752. .9118
rpt_family="MLT1B"
119. 97.1
                                                                                                                                                                                                                                                                                                                                                                                                                                          cpt_family="AluJo" | 160
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3780. .13803
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1305. .11342
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1859. .12212
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DEFINITION Homo sapiens chromosome 12 clone RP11-642P15, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 TGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 GCAACCTCCGCCTTCGCGCTTAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGAC 324
                                                                                                                                                                                                                                                                                                                                                                                   90 AGGTCAAGATCACGCAGCTAACAAATGAGCCAAGACTCTTGCTTTAGAGCTTGTCCTCTA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 CICIATICITICITICITICCAAAAACACIACAATITITIGITITIGITITIGITITIGITITIGITITIGITIT 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 126.4; DB 2; Length 110000;
Pred. No. 6.4e-22;
0; Mismatches 46; Indels 0;
                                                                                                                                                                                                             Length 184338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS AC009771 Accession AC009771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCGGGACACCACGTAAAAATGATCAAGTTCTAACATGTATGCATA 376
                                                                                                                                                                                                             25.7%; Score 128.6; DB 9; 65.5%; Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                0; Mismatches
/rpt_family="AluJo"
14374. .14663
/rpt_family="LIMB4"
14669. .15128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110000
210000
310000
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Best Local Similarity 77.0%;
Matches 154; Conservative (
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WPCOMMENT
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AC012386 0
WPCOMMENT
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SOURCE

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 24 conties. The true order of the pieces is not known and their order in this sequence record is
                                                            Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 346790 bases at least 040
Consensus quality: 34650 bases at least 030
Consensus quality: 349268 bases at least 020
Estimated insert size: 170200; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length contig of 7096 bp in length contig of 7096 bp in length gap of unknown length gap of unknown length contig of 9173 bp in length gap of unknown length contig of 10268 bp in length gap of unknown length contig of 10288 bp in length gap of unknown length gap of unknown length contig of 11237 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length
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gap of unknown length
contig of 22849 bp in length
gap of unknown length
contig of 27500 bp in length
contig of 34946 bp in length
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contig of 11012 bp in length
gap of unknown length
contig of 15635 bp in length
gap of unknown length
contig of 36174 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 2303 bp in length
gap of unknown length
contig of 3558 bp in length
contig of 3804 bp in length
gap of unknown length
contig of 3804 bp in length
contig of 2786 bp in length
gap of unknown length
gap of unknown length
contig of 2902 bp in length
gap of unknown length
contig of 4124 bp in length
contig of 4124 bp in length
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contig of 15546 bp in length
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contig of 10978 bp in length
aap of unknown length
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9 352304: contig of 36066 bp in length.
Location/Qualifiers
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contig of 5872
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/db_xref="taxon:9606"
/chromosome="12"
                     Sequencing vector: Plasmid;
Sequencing vector: M13;
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                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammaliai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alabrooks,S.L., Amaratunge,H.C., Arei,J.R., Ayele,M., Banks,T.,

Barbaria,J., Bonich, B., Brieker, C., Burcell, K.L., Bryank, N.P.,

Bubck,J., Bowie,S., Brieker, C., Burcell, K.L., Bryank, N.P.,

Bubay,C., Burch,P., Burkett,C., Covyle,M.D., Dathorne,S.R., David,R.,

Carron,T.F., Carter M., Cavazos,S.R., Chondry, J., Christopoulos,C.,

Cleveland,C.D., Cox,C., Covyle,M.D., Dathorne,S.R., David,R.,

Daviland,L., Davis,C., Davy-Carroll,L., Dederich,D.B.,

Delaney,K.R., Delgac,O., Denn,A.L., Ding,Y., Duthin, K.J.,

Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,

Falls,T., Ferraguco,D., Flagg,N., Ford,J., Foster, P., Franz,P.,

Garbis,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,

Garrell,J.H., Guevara,W., Gunarathe,P., Hale,S., Hamilton,K.,

Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Harnandez,J.,

Herrandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,

Jacobson,B., Jal,Y., Johnson,R., Holloway,C., Hollins,B.,

Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,J., Jackson,L.E.,

Jacobson,B., Jal,Y., Johnson,R., Molivey,C., Hollins,B.,

Jacobson,B., Howard,S., House,M., Golivet,S., Sudah,S.,

Marisson,E., Kally,S., Khan,U., Khig,L., Korvah,J., Kovar,C.,

Kratson,E., Kelly,S., Khan,U., Khig,L., Korvah,J., Kovar,C.,

Kratson,E., Kelly,S., Mhan,U., Khig,L., Korvah,J., Maksoy,B., Mawhiney,B., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Massoy,B., Mahminey,B., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Massoy,B., Martin,R., Martin,R., Martin,R., Martin,R., Massoy,B., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (27-0CT-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: HMPZ
Center clone name: RP11-642P15
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SEQUENCE, 24 unordered pieces.
                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT
                                           AC012386.36 GI:22474781
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148068 bp DNA linear PRI 02-MAY-2001

Human chromosome 14 DNA sequence BAC R-66E7 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.
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I (Dases I to 148068)

Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Levy, M., Eckenberg, R., Brulls, T., deBerardinis, V., Cruaud, C., Squencing of the human chromosome 14

Unpublished
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Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : R-603H7 (AC=AL109847) Downstream BAC (overlapping the SP6 end) : R-382E15 -------
                                                                                                                                                                    29761
                                                                                                                                                                                                                                                                                               29762 GCAACCTCCGCCTCCAGGTTCAAGAGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAC 29821
                                                                                                                                                                                                                                                                           324
                                                                                                                                      TTGTTTTGTTTTGTTT 204
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                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Web : www.genoscope.cns.fr)
On May 7, 2001 this seguence version replaced gi:13509291.
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                                                                      Length 110000
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Quality coverage: 8.50x in Q20 bases; sum-of-contigs
                   4540 others
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                                                                 Query Match 25.1%; Score 126.4; DB 2; Best Local Similarity 77.0%; Pred. No. 6.4e-22; Matches 154; Conservative 0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
/clone="RP11-642P15"
73601 c 73327 g 101345 t
                                                                                                                                    CTCTATTCTTGCTTTTCCAAAAAACACTACAATT
                                                                                                                                                                                                                                                                                                                                                                           29822 TACAGGCAAGCGCCACCACG 29841
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Range : bases
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Human chromosome 14 DNA sequence BAC R-382E15 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
AL355840
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 17991)
Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C.,
Sequenching of the human chromosome 14
Unpublished
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89216 TTTTTGTTTTGTTTTGTTTTTAGACAGAGTCTCGCTCTGTCACCCAGGCTGGAGT 89275
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Upstream BAC (overlapping the T7 end) : R-960H4
Downstream BAC (overlapping the SP6 end) : R-66E7 (AC=AL161871)
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On Jun 7, 2000 this sequence version replaced gi:7799397.
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Quality coverage: 9.72x in Q20 bases; sum-of-contigs
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Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                /clone lib="RPCI-11"
28188 c 25806 g 41094
                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                      Location/Qualifiers
1. .148068
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HTG; HTGS_ACTIVEFIN.
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Best Local Similarity 86.3%;
Matches 151; Conservative
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SHGC-9796 G11325
WI-30358 G24410.
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Homo sapiens chromosome 5 clone CTD-2044J15, complete sequence.
AC010366
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DOE Joint Genome Institute.

DOE Joint Genome Institute.

Submitted (15-5EP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 (bases 1 to 115396)

Does Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (09-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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1 (bases 1 to 115396)

DOB Joint Genome Institute and Stanford Human Genome Center.

Unpublished
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33215 c 36220 g 61553 t
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Location/Qualifiers
1. .179937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="R-382E15"
/clone lib="RPCI-11"
33688. .33899
/note="matching EMBL:N23600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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                            Overall quality chart
Range : bases
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2 (Dases 1 to 214139)
DOE Joint Genome Institute.
Direct Submission
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Direct Submission
Direct Submitter (26-00 Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced gi:9954660.
                                                          Direct Submission
Submitted (21-UUL-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14333753.
Draft Sequence Produced by DOE Joint Genome Institute
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 214139)

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4 (bases 1 to 115396)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Woulity: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.4.
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HOmo sapiens.
Homo sapiens
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31964 a 26247 c 25572 g 31613
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Center Project Name: 697863
Center clone name: CITB-H1_2183B18
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/db_xref="taxon:9606"
/chromosome="5"
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Center: Joint Genome Institute
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Cambridgeshire, CB10 15A, UK. E-mail enquirties:
humquery@sanger.ac.uk Clone requests: clonarequest@sanger.ac.uk
On Feb 11, 2002 this sequence version replaced gi:18643769.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
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Human DNA sequence from clone RP11-396D18 on chromosome 1, complete
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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77: gap of unknown.
91: contig of 6314 bp in length.
91: gap of unknown length.
96: contig of 1975 bp in length.
66: gap of unknown length.
6222: contig of 8356 bp in length.
1522: gap of unknown length.
8228: contig of 6706 bp in length.
91807: gap of unknown length.
91807: gap of unknown length.
100081: contig of 2379 bp in length.
100081: contig of 12514 bp in length.
112695: gap of unknown length.
112795: gap of unknown length.
112795: gap of unknown length.
127489: gap of unknown length.
127489: gap of unknown length.
1489: gap of unknown length.
1489: gap of unknown length.
17341: gap of unknown length.
17341: gap of unknown length.
17394: contig of 26053 bp in length.
17394: gap of unknown length.
17394: contig of 26053 bp in length.
17394: contig of 42645 bp in length.
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/clone_lib="CalTech human BAC library D"
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Pred. No. 8.5e-22;
0; Mismatches 32
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/chromosome="5"
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Matches 145; Conservative
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Direct Submission
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                   Consensus quality: 177232 bases at least Q40
Consensus quality: 190777 bases at least Q30
Consensus quality: 195469 bases at least Q30
Consensus quality: 195469 bases at least Q30
Estimated insert size: 121000; pulse field gel estimation
Estimated insert size: 210239; sum-of-contigs estimation
Quality coverage: 7.99 in Q20 bases; pulse field gel estimation
Quality coverage: 4.6 in Q20 bases; pulse field gel estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                      This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                        3: contig of 1232 bp in length
3: gap of unknown length
5: contig of 1158 bp in length
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1559: gap of unknown length
2521: contig of 1262 bp in length
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp; WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group; Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human chromosome 14 DNA sequence BAC C-2593121 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP11-396D18 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RP11-175B9 is at 72090 in this sequence. The true right end of clone RP11-572A16 is at 2000 in this
                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/HGP/Chri
RP11-396D18 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 208309)
Hellig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
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                                                                                                                                                                         Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On May 7, 2001 this sequence version replaced gi:12580631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following BAC sequence is oriented from the T7 to the SP6 e.
Upstream BAC (overlapping the T7 end) : R-1074012 (AC=AL049828)
Downstream BAC (overlapping the SP6 end) : R-34018
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Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J.
Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 TCTATTCTTGCTTTTCCTTTCCAAAAAACACTACAATTTTTTGTTTTTGTTTTGTTTTT
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Quality coverage: 5.83x in Q20 bases; sum-of-contigs
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0; Mismatches 39;
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Contact: SeqRef@genoscope.cns.fr
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On Jul 27, 2000 this sequence version replaced gi:8440040.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 153185)
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Homo sapiens chromosome 11 clone RP11-660B16, WORKING DRAFT
SEQUENCE, 40 unordered pieces.
AC073238
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Consensus quality: 138081 bases at least Q40 Consensus quality: 138081 bases at least Q30 Consensus quality: 141663 bases at least Q20 Insert size: 191000; agarose-fp Insert size: 1949285; sum-of-contigs Quality coverage: 2.76 in Q20 bases; sum-of-contigs Quality coverage: 2.76 in Q20 bases; sum-of-contigs
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HTG; HTGS PHASE1; HTGS_DRAFT.
HOmo sapiens.
Db 74122 TACAGGCACCTGCCACCATG 74103
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12653:
16052:
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KEYWORDS
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25.1%; Score 125.4; DB 2; Length 153185;
Best Local Similarity 72.6%; Pred. No. 1.1e-21;
Matches 162; Conservative 0; Mismatches 61; Indels 0;
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note="assembly_name:Contig44"
53320. .70085
'note="assembly_name:Contig45"
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5950. .59672
note="assembly_name:Contig42"
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note="assembly_name:Contig46"
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note="assembly_name:Contig48"
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89307. . 94087
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94188. . 99446
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note="assembly_name:Contig25"
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note="assembly_name:Contig37"
1860. .44973
note="assembly_name:Contig38"
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note="assembly_name:Contig39"
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/note="assembly_name:Contig40"
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note="assembly_name:Contig43"
note="assembly_name:Contig22"
499. .5572
note="assembly_name:Contig23"
                                           673. .7062
note="assembly_name:Contig24"
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181 TITITGITITGITITGITITGTTTTGAGACAGGGTCTCGAGGTGTCACCCCAGGCTGGAGT 240

121 AAGACTCTTGCTTTAGAGCTTGTCCTCTATTCTTGCTTTTCTTCCAAAAAACACTACAA 180

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Db 152735 GTAGTGGCGCGATCTCGGCTCACCAGCTCTGCCTCCGGGTTCACGCCGTTCTCCTGC 152794
241 GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCGATTCTCCTGC 300
                                                                                                                                                                  Db 152795 CTCAGGCTCCTGAGTAGCTGGGACTACAGGCACCTGGCACCAC 152837
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5565.337 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-564-805-21

US-09-564-805-21

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US-09-564-805-10

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Maximum Match 100%
Listing first 45 summaries
                                                                             nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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	ALIGNMENTS				
Seguence 15, Appl	US-08-194-088B-15	10596 1	1.6		45
ednence 1	-08-087-783A-	σ	1.6	48.2	44
15,	•	10596 1	1.6		43
15,	٠	059	1.6	48.2	42
ı,	US-09-620-925-1	•	1.6	48.2	41
'n	US-08-910-647-1		1.6	48.2	40
à	US-09-130-114-1		1.6	48.2	c 39
7	US-09-359-081-2		1.6	48.2	38
Sequence 2, Appl	US-09-050-863-2	2580 3	1.6	48.2	37
'n	US-09-249-585A-2	1926 4	1.6	48.2	36
Sequence 1, Appli		4411529 4	1.6 4	48.6	c 35
'n	US-09-564-805-5	51 4		51	34
8,	US-09-564-805-8	58 4	7.0	58	33
51,	US-09-389-341-51	2517 4	5.0	58.4	32
Sequence 51, Appl	US-09-315-794-51		2.0	58.4	31
	US-09-564-805-12	59 4	2.0	59	30
11,	9-564		2.0	59	29
sednence /, Appli			7.7	65	87

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GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtid H.F.
APPLICANT: Simard, Jacques
APPLICANT: Wriad Genetics, Inc.
ITILE OF INVENTION: Chromosone 17p_Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
ITILE OF INVENTION: Gene and a Paralog
ITILE OF INVENTION: Gene and a Paralog
ITILE OF INVENTION WUMBER: US/09/564,805
CURRENT FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SSCYIDAN ON SEQ ID NOS: 2.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 2958; Best Local Similarity 100.0%; Pred. No. 0; Matches 2958; Conservative 0; Mismatches
                      Sequence 3, Application US/09564805
Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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US-09-564-805-3
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241 CAGCGGGTAGCCGGGACTCGGGCGCGCGCTCTACGTCTTCTCCCGAGTTCAACCGGTATC 300 241 CAGCGGTAACCGGAACTCGGCGCGCGCGCTTTACGTTCTAACCGGTATC 300 241 CAGCGGTAACCGGAACTCGGCGCGCGCGCTAACTAACTCTAACTTAAACTGAAATAAACTGAAAATAAACTGAAAATAAACTGAAAATAAAACTGAAAAACTAAAAACTGAAAAAAAA	TITTCAACTIGGGGGGGGTTCAGAGAGTCAGGGGGGGGGG	GCCTGGACACATATTCCTCACACACACACTGGTCTAATGTTGGGGGCTTAAGTGGAA 4 GCTTGGACACATATTCCTCACACACACACACACACACACA	21 IGATICTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGACCTCCACAAC	481 TGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAACTGG 540 	11 CTGTGCGGCCCCACTCTGCCCCAGAATACGAGATGAAACCATGACAGTTTACCAGATCC	601 CCATACACAGTGAACAGAGGGAAAAGCACCATGGCAGAGTCCAGAAAGGCCTC 660	661 TCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAATGAGCCACACC 720	TTCCACATGGTGTTAGCCAGAGAAGGGGGTCAGGGACTCTTCCCTGGTCGTAGCTTTCA 	TCTGTAAGCTTCACTTAAAGAGAGAAACTTCTTGGTGCTCAAAGCAAAGGAGATGGGCC	TCCCAGTTGGGACAGCTGCCATCGCTCCTATGCTGCTGTCAAGGACGGGAAAAGCA 	TCACTCATGAAGGAAGAAGATTTTGGCTGAAGACTGTGTACTCCTCCAGATCCTGGTG 	CTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCA	CCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTGGTTCACATGG	1081 CCCCAGCATCTGTGGACAGCAGGTACCAGCAGTGGATGGA		1201 AGATTCAACCCAGCTCAACCTCACCGGACATCTTCCCCCTGCTGACCAGCAGTTTCC	GCTGTAAGAAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAATGCCTCCTCA
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AGGGATGCCATTATTACTTGCAATCCTG 1380 AAGATTCGAAATGTCAGTGCCACACTTG 1560 1620 1620 GECCEGGGCACCCEGGCTGCTGTTTG 1680 TTGCCAAGTATCTTGCTGCAGAGAAC 1740 CCTTTGCTGGTGGTTGCCCCCAACCAGC 1800 TGCCAGGAGGTCCTGCACCACATCAGTA 1860 GAGATCTCCAGTCCTGCAGTGGAAGAT 1920 GAAGAGTTTCAGACCTGTCTGGTGCGGC 1980 2040 CGGATGGGGAAAGATGCCACCCTCCTGA 2100 GAGGAAGCAGTGGAAAAGACACACAGCA 2160 ATGAACGCGGAGTTCATTATGCTGAACC 2220 TTCAGCCCCAACTTCAGCGAGAAAGTGG 2280 GGGGGCTTTCCAACAATGCCCAAGCTGA 2340 ATCGAGGAGATGGAGGAGCGCAGGGAGA 2400 AACTTCCAGCAGAGCGTGCAGGAGTACA GAGAAAGAAGTCAGTACCCAGAAATCA CACACCTCTGGCTGGAAAGTGGTCTATT GACTGTGGTGAGGGCACATTTGGGCAGC

CTGTCCAGGGAGCTGGCAGGCGGCCTGG 2460

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APPLICANT: Tavidjan, Sean V.
APPLICANT: Tavidjan, Sean V.
APPLICANT: Tavidjan, Sean V.
APPLICANT: Tang, David H.F.
APPLICANT: Rommens, Joaques
APPLICANT: Rommens, Joaques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US 60/107,468
FRIOR TAILING DATE: 1998-11-06
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1998-11-05
FRIOR FILING DATE: 1999-11-05
FRIOR FILING DATE: 1999-11-05
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 223
LENGTH: 2908
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               AGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCAGGCGGCCCTGG
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97.2%; Score 2874.4;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches
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Patent No. 6333403
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TAAAGATTGAGTTTGCAA 2958
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ORGANISM: Pan troglodytes
FEATURE:
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; LOCATION: (1)
US-09-564-805-223
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US-09-564-805-223
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Sequence 225, Application US/09564805

Sequence 225, Application US/09564805

Ratent No. 633403

GENERAL INFORMATION:

APPLICANT: Tartigian, Sean V.

APPLICANT: Simard, Jacques

APPLICANT: Simard, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Cene and a Paralog and Orthologous Genes

TITLE REPERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/564,805

CURRENT FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: Patentin Ver. 2.0 2450 2510 2640 2700 2810 CCCAAGCTGATTCCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGGGAGATGGAGGAG 2521 CTGCCCCACGCACGCACCCCCTATCTGCCCTCCTTGCTGGAAGACTGAAGAGCACGGTC GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAACATTTGCAACAATG CGCAGGAGAAAGCGGGGAGCTGCGGCAGGTGCGGGCCCTCCTGTCCAGGGAGCTGGCA AAGAAGGTCAGAGCCCAGTGAAGATCTGGGAGACCCTGAATTCAGAAGGCTGTGTGTTTT AAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCCTGGCACAGCCGCGGGCCAAGGAGG GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG cecagedagaaecegeaacrecegeaagarecegecegecererereaeaaagareeaa GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCCACACAGAGGAGCCACACAGGCC CCCCAGGAGGCAGCTCAGGATAGGTGGTATGGAGCTGTGCCGAGGCTTGGGCTCCCAAT AAGAAGGTCAGAGCCCAGTGAAGATCTGGGAGACCCTGAACTCAGAAGGCTGTGTGTCTT CTGCCCCACGCACGCACCCGTATCTGCCTCCTTGCTGGTAGAAGCTGAAGAGCACGGTC

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Matches 2863; Conservative
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                    ; TYPE: DNA
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; FEATURE:
; NAWE/KEY: CDS
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US-09-564-805-225
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Sequence 1, Application US/09564805; Patent No. 633403; GENERAL INFORMATION: APPLICANT: Teng, David H.F. APPLICANT: Simard, Jacques; APPLICANT: Rommens, Johanna M.

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APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
FILE REFERENCE: 2318-258
CURRENT PAPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1000-05-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: 1999-11-05
SEQ ID NO 1
LENGTH: 2481
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83.9%; Score 2481; E
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches
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; LOCATION: (1)..(2478)
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; TYPE: DNA ; ORGANISM: Mus musculus	AAGGGGCTGAGTCTCCAGTCCTGCA	
; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 221 ; LENGTH: 2470	OY 1791 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACACACCAGGAGGTCCTGCAC 1850	
; PRIOR FILING DATE: 1998-11-06 ; PRIOR APPLICATION NUMBER: 09/434,382 ; PRIOR FILING DATE: 1999-11-05 . MIMPER OF SECT TO NOC: 240	OY 1731 CAGAGAGACCCGCCTTGGCAACTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCTGC 1790	
CURRENT APPLICATION NUMBER: US/09/564,805 CURRENT FILING DATE: 2000-05-05 PRIOR APPLICATION NUMBER: US 60/107,468	1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG	
; APPLICANT: Myriad Genetics, Inc. ; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Ca ; TITLE OF INVENTION: Gene and a Paralog and Orthologov	Db 1561 TITGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGGCT 1620 Ov 1671 GCTGTGTTTGTGTCCCACTGCACGAGACCAGGTGGACAGGGTCCTAGGGCAACCTGGGCT 1620	
; APPLICANT: Simard, Jacques ; APPLICANT: Romens, Johanna M.	TTTGGGCAGCTCTGCCGTCATTACGGAGACCAGGTGGACACGGGCACCTGGCT 1	
; GENERAL INFORMATION: ; GENERAL INFORMATION: ; APPLICANT: Tavijd H.F.	QY 1551 GCCACACTTGTCAACATAAGCCCCGACACGTCTGCTACTGGACTGTGGTGGGGGCACA 1610 Db 1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTTGCTACTGGACTGTGGTGAGGGCACA 1560	
що	QY 1491 CCAGAAATCATCTTGGAACAGGATCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1550 Db 1441 CCAGAAATCATCTTGGAACAGGGTCTGCCATGAAGATTCGAATGTCAGT 1500	
DD 2461 AAGAAGGTCAGGGA 2531	QY 1431 CAGGAGTACAGGAGGAGGACGAGCCCAGCCCAGCAGAGAAAAAAAGAAG	
2451	Qy 1371 IGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGGGTG 1430 Db 1321 IGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380	
2391	OY 1311 TGCCTCCTCAAGTACCAGCTCCGTCCGAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1370	
Oy 2331 CCCAAGCTCATTCCCCACTGAAAGCCCTGTTTGCTGGCGACATCG	OY 1251 ACCAGTTTCCGCTGTAAGAAGAGGCCCCACCTCAGTGTGCCCATGGTTCAGGTGAA 1310	
Oy 2271 GAGAAAGTGGGAGTTGCCTTTGACCATGAAGGTCTGCTTTGAGAG	Qy 1191 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1250 Db 1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200	
Oy 2211 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCTCTTCAC Db 2161 ATGCTGACCACTTCAGCCAGCGCTATGCCAAGGTCCCCTCTTCA	Qy 1131 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCT 1190 Db 1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140	
Qy 2151 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGA.	dy 1071 GTTCACATGGCCCCAGCATCTGTGGACAGCAGGTACCAGCAGTGGATGGA	
2091	Qy 1011 TGTGAGAATGCCACCTTTCAGAGGTACCAAAGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1070 D 961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020	
Oy 2031 GTGGTCTATICCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGA	QY 951 GATCCTGGTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATCCATC	
Oy 1971 CTGSTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACACA	OY 891 GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTGTACTCCTCCA 950 Db 841 GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900	
Qy 1911 GTGGAAGATTGATCAGTTGCGTGCGAACATGTCATTTGGAAG.	Qy 831 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 890 Db 781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCATCATTGCTGCTGTCAAGGAC 840	
	OY 771 GTAGCTTTCATCTGAAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 830 Db 721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAAGAACTTCTTGGTGCTCAAAGCAAAG 780	

Cancer Susceptibility yous Genes ATGGGAAAGATGCC 2090 AACGCGGAGTTCATT 2210 AGCCCCAACTTCAGC 2270 AGACTTTCCAACAATG 2330 GAGGAGATGGAGGAG 2390 ||||||||||||||||| |GAGGAGATGGAGGAG 2340 :ACCTCTGGCTGGAAA 2030 ||||||||||||||||||| |ACCTCTGGCTGGAAA 1980

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OTHER INFORMATION: positions 22211 and 23879 is
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Sinard, Jacques
APPLICANT: Sinard, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
NUMBER OF SEQ ID NOS: 240
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AGCGAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACA
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Patent No. 6333403
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ORGANISM: Homo sapiens
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APPLICANT: Tavtigi
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LENGTH: 26664
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APPLICANT: Teng, David H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPRENCE: 2118-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT PRILING DATE: 2000-05-05
PRIOR PEPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
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Score 657.2; DB 4;
Pred. No. 9.6e-167;
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Patent No. 6333403
22.2%;
Query Match 22.2
Best Local Similarity 99.5
Matches 659; Conservative
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Rommens, Johanna M.
Myriad Genetics, Inc.
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; LOCATION: (51)..(293)
US-09-564-805-210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTCTGCTTTGGAGACTTTCCAACAATGCCCAAGCTGATTCCCCCCACTGAAAGCCCTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.1%; Score 655; DB 4; Length 655; 100.0%; Pred. No. 5.2e-167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
| PRIOR APPLICATION NUMBER: 09/434,382 |
| PRIOR FILING DATE: 1999-11-05 |
| NOMBER OF SEQ ID NOS: 240 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SEQ ID NO 27 |
| LENGTH: 655 |
| TYPE: DNA |
| PRATURE: |
| PRATURE: |
| NAME/KEY: misc_feature |
| LOCATION: (1)..(228) |
| OTHER INFORMATION: exon 24 |
| NAME/KEY: POlyA_signal |
| LOCATION: (456)..(641) |
| US-09-564-805-27 |
| NAME/KEY: (456)..(641) |
| US-09-564-805-27 |
| PRIOR PRIOR NUMBE/KEY: POLYA_signal |
| US-09-564-805-27 |
| PRIOR INFORMATION: (456)..(641) |
| PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR P
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US-09-564-805-210
Sequence 210, Application US/09564805
Sequence 210, Application US/09564805
GENERAL INFORMATION:
APPLICANT: Taravigian, Sean V.
APPLICANT: Taray, David H.F.
APPLICANT: Simard, Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 655; Conservative
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Best Local :
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us-uy-564-805-4
; Sequence 4, Application US/09564805
; Patent No. 6333403;
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFRENCE: 218-258
; CURRENT FILING DATE: 2000-05-05
; PRIOR PAPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1999-11-05
; RIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes FILE REPERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR PILING DATE: 1999-11-06
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 210
LENGTH: 350
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Sequence 26, Application US/09564805
; Sequence 26, Application US/09564805
; Batent No. 6333403.
; GENERAL INFORMATION:
    APPLICANT: Tavtigian, Sean V.
; APPLICANT: Tavtigian, Johanna M.
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Generics, Information of Inventions Generics, Information of Inventions Generics, Information of Invention Generics, Information of Inventions Generics, Information of Inventions Generics, Information of Invention of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Information of Informat
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                                                                                                                                                                                                                                            121 AGTTAAAGGTTGCTCGCCTGGACAACATATTCCTGACAAGGAATGCACTGGTCTAATGTTG 180
                                                                                                      61 AGTTCAACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACA 120
                                                                                                                                                                             AGTTAAAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTG 405
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Pred. No. 7.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.9%; Score 145; DB Best Local Similarity 100.0%; Pred. No. 7.76
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Patent No. 633403
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tang, David H.F.;
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.;
TITLE OF INVENTION: Chromosome 17p-Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2279 GGGAGTTGCCTTTGACCACATGAAG 2303
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| LOCATION: (1)...(145)

| OTHER INFORMATION: exon 23

US-09-564-805-26
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTGCAGGTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
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APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia B.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCC-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-108
EARLIER FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 315
LENGTH: 238
                                                                                                                                                                                                                                                                                                        Query Match 10.0%; Score 295; DB 4; Length 295; Best Local Similarity 100.0%; Pred. No. 4e-70; Matches 295; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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100.0%; Pred. No. 1.6e-54;
Live 0; Mismatches 0;
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Patent No. 6262333
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 237; Conservative
                                                                                               PEATURE:
NAME/KEY: misc_feature
LOCATION: (51)...(295)
US-09-564-805-4
                                   TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-328-111-315
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LENGTH: 295
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ORGANISM: Homo sapiens
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US-09-564-805-10
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US-09-564-805-24
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Simard, Joaques
APPLICANT: Rommens, Joaques
APPLICANT: Rommens, Joaques
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: UNMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FLING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 20
LENGTH: 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1130 GTTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCT 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes; FILE REFERENCE: 2318-258; CURRENT PAPLICATION NUMBER: US/09/564,805; CURRENT FILING DATE: 2000-05-05; PRIOR PILING DATE: 1998-11-06; PRIOR PILING DATE: 1998-11-06; PRIOR FILING DATE: 1999-11-05; NUMBER OF SEQ ID NOS: 240; SEQ ID NOS: 240; SEQ ID NO 16; SEQ ID NO 16; LENGTH: 139
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Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 139; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.7%; Score 139; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 139; Conservative 0; Mismatches 0;
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LOCATION: (1)...(139)

CTHER INFORMATION: exon 17

US-09-564-805-20
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; OTHER INFORMATION: exon 13
US-09-564-805-16
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (1)...(139)
                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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US-09-564-805-20
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Sequence 24, Application US/09564805

Sequence 24, Application US/09564805

Patent No. 6333403

GENERAL INFORMATION:

APPLICANT: Tang, David H.F.

APPLICANT: Feng, David H.F.

APPLICANT: Formans, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

CURRENT APPLICATION NUMBER: US/09/564,805

CURRENT APPLICATION NUMBER: US 60/107,468

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PatentIn Ver. 2.0

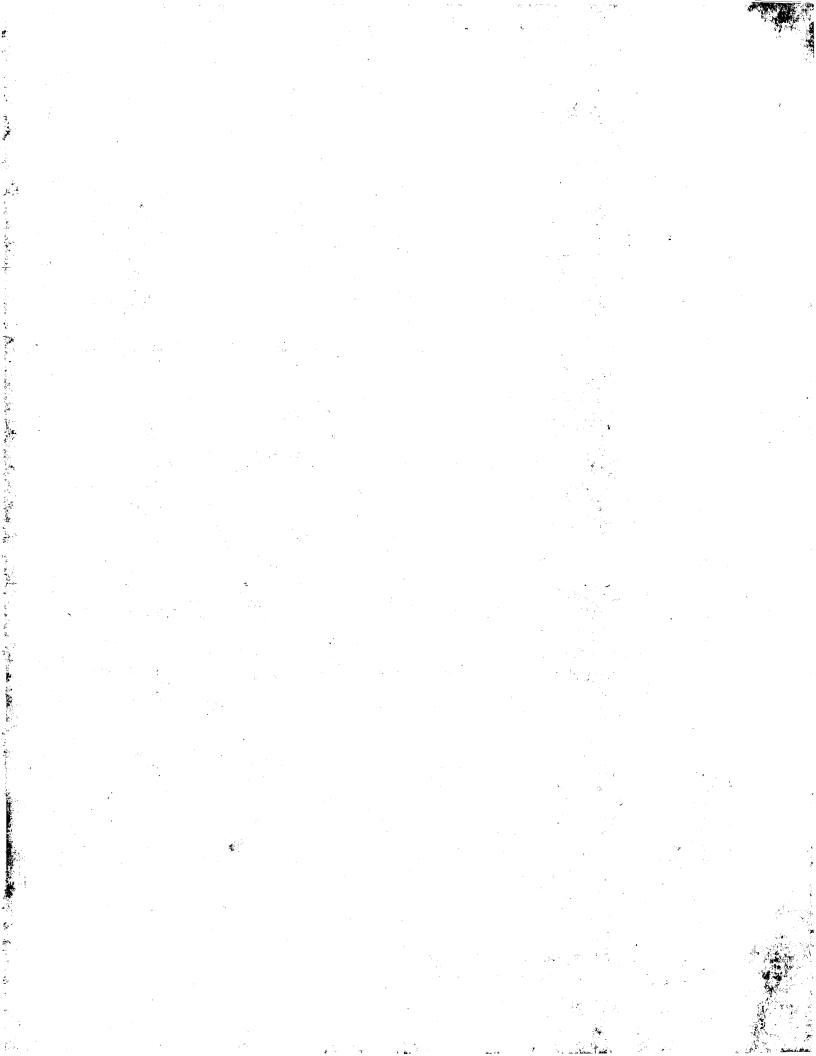
SEQ ID NO 24

LENGTH: 121

TYPE: DNA
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Patent No. 633403
GENERAL INFORMATION; Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1959 TTTCAGACCTGTCTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACC 2018
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                                                                                                                            61 TTACGGAGACCAGGTGGACAGGCTCCTGGGCACCCTGGCTGTTTTGTGTCCCACCT 120
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100.0%; Pred. No. 2.1e-23;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                      1691 GCACGCAGATCACCACACG 1709
                                                                                                                                                                                                                                     121 GCACGCAGATCACCACACG 139
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Best Local Similarity 100.0
Matches 121; Conservative
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| LOCATION: (1)...(121)
| OTHER INFORMATION: exon 21
US-09-564-805-24
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| CURRENT APPLICATION NUMBER: US/09/564,805
| CURRENT FILING DATE: 200-05-05
| PRIOR APPLICATION NUMBER: US 60/107,468
| PRIOR FILING DATE: 1998-11-06
| PRIOR FILING DATE: 1998-11-05
| PRIOR FILING DATE: 1999-11-05
| SEQ ID NOS: 2-0
| SEQ ID NOS: 2-0
| SEQ ID NOS: 2-0
| SEQ ID NOS: 2-0
| TYPE: DNA
| ORGANISM: Homo sapiens
| FATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE: PATURE:
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Search completed: May 18, 2003, 00:09:50 Job time: 249 secs



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May 18, 2003, 00:09:53 ; Search time 359 Seconds (without alignments) 10628.516 Million cell updates/sec
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2958
1 cgcgggcgtaggtgaccggc.....aataaagattgagtttgcaa 2958
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO0_NSW PUB.seq:*
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     810007 segs, 644969091 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3, Appli	Sequence 3, Appli	223	Sequence 223, App	Sequence 225, App	Sequence 225, App	Sequence 1, Appli	٦,	N	Sequence 221, App	Sequence 2039, Ap	Sequence 28, Appl	Sequence 28, Appl		Sequence 27, Appl	2	Sequence 8996, Ap	Sequence 210, App	Sequence 210, App
ΩI	US-09-988-626-3	US-09-988-687-3	US-09-988-626-223	US-09-988-687-223	US-09-988-626-225	US-09-988-687-225	US-09-988-626-1	US-09-988-687-1	US-09-988-626-221	US-09-988-687-221	US-09-833-381-2039	US-09-988-626-28	US-09-988-687-28	US-09-988-626-27	US-09-988-687-27	US-09-833-381-2038	US-09-918-995-8996	US-09-988-626-210	US-09-988-687-210
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% Query Match	100.0	100.0	97.2	97.2	95.3	95.3	83.9	83.9	55.6	55.6	24.8	22.2	22.2	22.1	22.1	15.9	14.6	10.1	10.1
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111	NESULT 1 US-09-988-626-3 Sequence 3, Application US/099886; Bedblication No. US20030044959A1 GENERAL INFORMATION: APPLICANT: Tavtigian, Sean V. APPLICANT: Tavtigian, Sean V. APPLICANT: Tavtigian, Jacques APPLICANT: Rommens, Johanna M. APPLICANT: Myriad Genetics, Inc. TITLE OF INVENTION: Gene and a FILE REFERENCE: 2318-258 CURRENT FILING DATE: 200-05-05-05 PRIOR PRIOR PELICATION NUMBER: US/07 CURRENT FILING DATE: 200-05-05-05 PRIOR PRIOR DATE: 1998-11-06 PRIOR PLILING DATE: 1998-11-06 PRIOR FILING DATE: 1998-11-06 PRIOR FILING DATE: 1998-11-06 PRIOR FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 240 SSOFTWARE: Patentin Ver: 2.0 SSOFTWARE: Patentin Ver: 2.0 SSOFTWARE: Patentin Ver: 2.0 SSOFTWARE: Patentin Ver: 2.0 SSOFTWARE: Patentin Ver: 2.0 SCALURENT: HOMO Sapiens FEATURE: NAME/KEY: misc feature LOCATION: (51)-(5531) OTHER INFORMATION: coding sequence	L L SC M
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Publication No. US20030045704A1

GENERAL INFORMATION:

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Binard, Jacques

APPLICANT: Rommens, Johanna M.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,687

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 1998-11-06

PRIOR APPLICATION NUMBER: 09/564,805

PRIOR FILING DATE: 1999-11-06

PRIOR APPLICATION NUMBER: 09/544,382

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51)..(2531)
OTHER INFORMATION: coding sequence as in SEQ ID
US-09-988-687-3
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100.0%; Score 2958;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2958; Conservative 0; Mismatches
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RESULT 3

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Pred. No. 0;
0; Mismatches
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ilarity 99.3%;
Conservative
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ORGANISM: Pan troglodytes
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Best Local Similarity
Matches 2887; Conserv
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Sequence 223, Application US/09988687

Sequence 224, Application Wo. US20030045704A1

GENERAL INFORMATION:

APPLICANT: Tavitidan. Sean V.

APPLICANT: Simard, Jacques.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Ghromosome 17p-Linked Prostate Cancer Susceptibility

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TUTLE OF INVENTION WIMBER: US/09/988,687

CURRENT FILING DATE: 1209-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-05

SEC ID NO 223

LENGTH: 2088

TWANTER PATENTION WIMBER: DATE: 1999-11-05

LENGTH: 2088

TWANTER PATENTION WIMBER: DATE: 1999-11-05

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Best Local Similarity 99.3%;
Matches 2887; Conservative
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ORGANISM: Pan troglodytes
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Fublication No. US20030044959A1
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Sommens, Johanna M.
APPLICANT: Sommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT APPLICATION NUMBER: US/09/988,626
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Matches 2863; Conservative (
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US-09-988-626-225
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Query Match
Best Local Similarity 98.5%;
Matches 2863; Conservative
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ORGANISM: Gorilla gorilla
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Sequence 225, Application US/0998687

Publication No. US20030045704A1

GENERAL INPORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Johann N.
APPLICANT: Tavtigian, Johann M.
APPLICANT: Teng, David H.F.
APPLICANT: Romens, Johann M.
APPLICANT: Romens, Johann M.
APPLICANT: Romens, Johann M.
APPLICANT: Romens, Johann M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT FILING DATE: 2001-11-20
PRIOR PELICATION NUMBER: US/09/54,805
PRIOR FILING DATE: 1998-11-06
PRIOR PELING DATE: 1998-11-06
PRIOR PELING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0 2750 2744 2684 2804 Gaps TTGGAAACAGACGGCAGCACCTTTCCTCTAATCCAGCAAAGTGATTCCCTGCACACCAGA GACAAGCAGAGTAACAGGATCACTGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATT CTGCCCCACGCACGCACCCGTATCTGCCCTCCTTGCTGGTAGAAGCTGAAGAGCACGGTC GACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACGAAATAGTATT GCCGCCTGGAGGATGGGGAGCCTCAGCAGAAACGGCCCACACAGAGAGGAGCCACAGAGCC AAGAAGGTCAGAGCCCAGTGAAGATCTGGGAGACCCTGAATTCAGAAGGCTGTGTGTCTT CTGCCCCACGCACGCACCCGTATCTGCCCCTCCTTGCTGGTAGAAGCTGAAGACACGGGTC CCCCAGGAGGCAGCTCCAGGATAGGTGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACAT AAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCCTGGCACAGCCGCGGGGCCAGGAGG TTGGAAACAGACGCGCCACCTTTCCTCTAATCCAGCAAAGTGATTCCCTGCACAGA AAGAAGGTCAGAGCCCAGTGAAGATCTGGGAGACCCTGAACTCAGAAGGCTGTGTGTCTT 16; Length Indels o, .. 29; DB Score 2819.6; Pred. No. 0; 0; Mismatches 2958 2865 TCAGCTGCAATAAAGATTGAGTTTGCAA 2892 TCAGCTGCAATAAAGATTGAGTTTGCAA

SCGCTTTGCTGCTGCTGCGGCCGGGCGGACGCACCATGTCGCAGGGACGC		TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCCAAAGTGTGTACTTTCTGGA	TACCAGATCCCCATACACACTCCACTCCCCCAAAAAACCATGACAATTACAAAAACATTACAAAAACATTACAAAAACATTACAAAAACAAC	661 GAGCCACACCTTCCACATGGTGTTTAGCCAGAGAGGGGTTTTTTTGTTCCTTGGTC 720 771 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGGGTTCTTGGTGCTCAAAGCAAAG 830 721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGAAACTTCTTGGTGCTCAAAGCAAAG 780 831 GAGATGGGCCTCCCAGTTGGAACTGCCATCGTTCATGGTGCTGTCAAGGAC 721 GAGATGGGCCTCCCAGTTGGAACAGCTGCCATCCATCATTGCTGCTGTCAAGGAC 890 781 GAGATGGGCTTCCCAATTGGAACAGCTGCCATCGTTCATTGCTGCTGTCAAGGAC 840	91 GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 95	1011 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAGGCAGATGCCCCGGTGGCCTTGGTG 1070
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TYPE: DNA
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GENERAL INFORMATION:

APPLICANT: Tartigian, Sean V.

APPLICANT: Teng, David H.F.

APPLICANT: Simard, Jacques

APPLICANT: Rommens, Jocques

APPLICANT: Rommens, Johanna M.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: WABER: US/09/988,626

CURRENT APPLICATION NUMBER: 2001-11-20

PRIOR APPLICATION NUMBER: 09/564,805

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-05
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Publication No. US20030044959A1
GENERAL INFORMATION:
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	Db 1981 GTGGTCTATTCCGGGGACACCACGCGAGG	Oy 2091 ACCCTCGATACATGAAGCCACCCTGGAAGATG	QY 2151 ACACACAGCACAAGGTCCCAAGCCATCAGCGTGG	2101	Db 2161 ATGCTGAACCACTTCAGCCAGCCTATGCCAAGC	Qy 2271 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGG	Db 2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTC	Oy 2391 CGCAGGGAAACGGGAAGCTGCGGCAGGTGCGGC	Dy 2451 GCCGCCTGGAGGATGGGGAGCTCAGAGAGGGGAGAGGGGGGGG	Oy 2511 AAGAAGGTCAGAGCCCAGTGA 2531 	RESULT 8 US-09-988-687-1 ; Sequence 1, Application US/0998687	GENERAL INFORMATION: ; APPLICANT: Tavtigian, Sean V. ; APPLICANT: Tang, David H.F.	APPLICANT: SIMERIA, JACQUES APPLICANT: Rommens, Johanna M. APPLICANT: Myriad Genetics, Inc. ITLE OF INVENTION: Chromosome 17p-Linked	FILE REFERENCE: 2318-258 ; CURRENT APPLICATION NUMBER: US/09/988,687 ; CURRENT FILING DATE: 2001-11-20	FRIOR FILING DATE: 2000-05-05 PRIOR PILING DATE: 2000-05-05 PRIOR APPLICATION NUMBER: US 60/107,468 PRIOR FILING DATE: 1998-11-06 PRIOR FILING DATE: 1998-11-06	FILOR AFELLANDIN NOWBER: 09/494,382 FRIOR FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 240 SOFFWARE: Patentin Ver. 2.0	; SEQ 1D NO 1 ; LENCTH: 2481 ; TYPE: DNA ; ORGANISM: Homo sapiens	S-0	Query Match 83.9%; Score 2481 Best Local Similarity 100.0%; Pred. No. Matches 2481; Conservative 0; Mismatc
841 GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900	951 GATCCTGGTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCA	TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG	1 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG	1071 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGA	1131 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1190 1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACTT 1140	1 GCAGCCACAAGATTCAAACCCAGGTCAACCTCATCCACCGGGACATCTTCCCCTGCTC	ACCAGTITCCGCTGTAAGAAGGAGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA	TGCCTCCTCAAGTACCAGCT TGCCTCCTCAAGTACCAGCT	1 TGCAATCCTGAGGAATTCAT	CAGGAGTACAGGAGGAGTGC 	1491 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1550 	1551 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1610	1611 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1670	1671 GCTGTGTTTGTGTCCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1730 	1731 CAGAGAGAACGCGCCTTGGCAICTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1790 	1791 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGGGGGGGG	1851 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1910 	1911 GTGGAAAGATTGATCAGTTCGCGTACCAACATGTGATTTGGAAGGTTTCAGACCTGT 1970 	1971 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGG
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APPLICANT: Tavtigian, San V.
APPLICANT: Tavtigian, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Somens, Johanna M.
APPLICANT: Somens, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
FILE REFERENCE: 218-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 221
LENGTH: 2470
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Pred. No. 0;
0; Mismatches
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Matches 1958; Conservative
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APPLICANT: Taviidan, Sean V.
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APPLICANT: Taviidan, Sean V.
APPLICANT: Taviidan, Sean V.
APPLICANT: Taviidan Sean V.
APPLICANT: Simard, Joaques
APPLICANT: Rommens, Joaques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-238
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT APPLICATION NUMBER: US/054,805
PRIOR PILING DATE: 2000-05-05
PRIOR PRILOR DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver: 2.0
SEC ID NO 221
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Pred. No. 0;
0; Mismatches 417; Indels
                                                                      Sequence 221, Application US/09988687
Publication No. US20030045704A1
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Best Local Similarity 81.6%;
Matches 1958; Conservative
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                                                                                                      GENERAL INFORMATION:
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; LOCATION: (1)
US-09-988-687-221
                                                    US-09-988-687-221
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Nucleic Acid and Protein Homologs 2239 GTGCCCAAGCTGATTCCCCCACTGAAGGCCCTGTTTGCAGGTGACATTGAAGAAGAGATGGTG 2298 2448 GCAGGCGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCCACA 2506 2356 GCAGACACCCCAGAGGACAGAGAACCCCAACAGAAGCGGGCCCACACAGATGAACCACA 2414 CTGCAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTT 1699 GCTCCTACCCAGCTCAGGGCCTGGCTGCAGCAGTATCACAACCACTGCCAGGAGATTCTG CACCACGTCAGTATGATTCCTGCCAAATGCCTTCAGAAAGGGGCAGAGGTCTCCAATACT 1819 ACATTGGAAAGGCTGATAAGCTTGCTGTTGGAACATGTGACTTAGAAGAATTTCAGACC GCCACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAA 1999 GCCACCTCCTGATACATGAAGCCACTCTGGAGGATCNCTTGGAAGAGGAAGGAGTAGAG AAGACACACACACACAACGTCCCAAGCCATCAGCGTGGGGATGCGGAACGCGGAGTTC AGGACACACAGCACCTCCCAGGCTATTAATGTGGGGATGCGGATGAATGCGGAGTTC 2208 ATTATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTC ATCATGCTGAACCACTTCAGTCAGCGGTACGCNAAGATCCCCCTTTTTCAGCCCTGACTTC ATGCCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAG 2299 GAACGCAGGGAGAAAAAGGGAGCAACGCTGCTGCGAGCAGCAGCACCTCTGACC ---CAGCAG GCCCCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTG CACCACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGGCTGAGATCTCCAGTCCT GCAGTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACC AAAGTGGTCTATTCCGGGGACACCCTGCCTGCGAGGCTCTGGTCCGGATGGGGAAAGAT AGCGAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACA Sequence 2019, Application US/09833381
Patent No. US20020132090A1
GENERAL INPORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090A1e1 Nuc
FILE REFRENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2039 TYPE: DNA ORGANISM: Homo sapiens NAME/KEY: misc feature -09-833-381-2039 1639 1788 1759 1908 1968 2028 1939 2088 2148 2059 2119 2268 2179 2328 1848 1728 g g g Db Db Db g ò - 6 ò qq à g ò ОР g ò g ò ò ò ò ò δ ò 8

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APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT PAPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR PLING DATE: 1998-11-06
PRIOR PELING DATE: 1998-11-06
PRIOR PELING DATE: 1998-11-05
PRIOR PELING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 26664
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ORGANISM: Homo sapiens
FATURE:
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Pred. No. 2e-196;
0; Mismatches 3; Indels
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Best Local Similarity 99.5%;
Matches 659; Conservative C
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                                                                                       Score 734.8; DB 10
Pred. No. 6.7e-222;
0; Mismatches 10;
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US-09-988-626-28
US-09-988-626-28
Sequence 28, Application US/09988626
Publication No. US20030044959A1
GENERAL INFORMATION:
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
                              Ö
                              or
                                                                                       Query Match
Best Local Similarity 98.3%;
Matches 772; Conservative
                          = A,T,C
      ; LOCATION: (1)...(783)
; OTHER INFORMATION: n
US-09-833-381-2039
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ORCANISM: Homo sapiens
FEATURE:
FRATURE:
COCATION: (910)...(13104)
OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
OTHER INFORMATION: 9186-8244; exon 9: 12878-12936; exon 10:
OTHER INFORMATION: 13032-13104;
NAME/KEY: misc_feature
COCATION: (13756)...(12917)
OTHER INFORMATION: 13: 16278-16416; exon 12: 15283-15378; exon 10:
OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:
OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:
OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
NAME/KEY: misc_feature
COCATION: (23045)...(2645)
COCATION: (23045)...(2645)
COCHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon 21: OTHER INFORMATION: exon 19: 22073-220375; polyadenylation
OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation
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 CCCTCCTTGCTGGTAGAAGCTGAAGAGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTG 26164
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APPLICANT: Tavidian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptis
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptis
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptis
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptis
TITLE OF INVENTION: 2010-11-20
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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US-09-988-687-28
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Publication No. US20030044959A1
GENERAL INFORMATION:
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Romanns, Johanna M.
APPLICANT: Romanns, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
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OTHER INFORMATION: signal: 26447-26452

NAME/KEY: variation

LOCATION: (826)...(23879)

OTHER INFORMATION: s at positions 826 and 23180 is G or C; y at OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486

OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at OTHER INFORMATION: positions 22211 and 23879 is A or G.
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Sequence 27, Application US/09988687
Publication No. US20030045704A1
GENERAL INFORMATION:
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Matches 655; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (1). 7(228)
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (636)..(641)
US-09-988-687-27
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; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes; FILE REFERENCE: 2318-258; CURRENT APPLICATION NUMBER: US/09/988,626; CURRENT FILING DATE: 2001-11-20; PRIOR FILING DATE: 2001-05-05; PRIOR PLICATION NUMBER: 09/564,805; PRIOR PLICATION NUMBER: 09/564,805; PRIOR PLICATION NUMBER: 09/564,805; PRIOR PLICATION NUMBER: 09/434,382; PRIOR PLING DATE: 1999-11-05; PRIOR PLING DATE: 1999-11-05; PRIOR PLING DATE: 1999-11-05; PRIOR PLING DATE: 1999-11-05; PRIOR PLING DATE: 1999-11-05; PRIOR PLING DATE: 200-11-05; SOFTWARE: Patentin Ver: 2.0
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LOCATION: (1). [228)

OTHER INFORMATION: exon 24

NAME/KEY: polyA_signal

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Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt Lake City, UT 84108, USA
Location/Qualifiers
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Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A. A candidate prostate cancer susceptibility gene at chromosome 17p Nat. Genet. 27 (2), 172-180 (2001)
                                                                                                                                                                                                                               Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B. Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., and Cannon-Albright, L.A.
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Novel nucleic acids and polypeptides
Patent: WO 0222660-A 240 21-MAR-2002;
HYSEQ, INC. (US)
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                     241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAGTTA 300
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: i Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621.
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2997)

                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                        protein,
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Contact: MGC help desk
mail: egapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
BC Cancer Agencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                    BC001939 2997 bp mRNA linear PR Homo sapiens, putative prostate cancer susceptibility clone MGC:4102 IMAGE:2820640, mRNA, complete cds.
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BC001939.1 GI:12804972
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SOURCE
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ASLGKPLHPLLVVAPNQLKAWLQQYHNQCQEVLHHISMIPAKCLQEGAEISSPAVERL
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b 853

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360 360 420 420 480 480 900 9 099 9 720 780 900 Gaps 9 61 ATGTGGGCGCTTTGCTCGCTGCTGCGCCGCGCGCGGACGCACCATGTCGCAGGACGC ACCATATCGCAGGCACCCGCCGCCGCGCGCGCGCGCGCAAGGACCCGCTGCGGCACCTG ACCATATCGCAGGCACCCGCCGCCGCGGGCCGCCGCCAAGGACCCGCTGCGGCACCTG CGCACGCGAGAGAGCGCGGACCGTCGGGGGTGCTCCCGGCGCCCAAACACCCGTGTACCTG GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGAGAACTTCTTGGTGCTCAAAGCAAAG GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTCTCAAGGAC 1 ATGTGGGCGCTTTGCTCGCTGCTGCGGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC CGCACGCGAGAGCGCGGGACCGTCGGGGGTGCTCCGGCGCCCAAACACGTGTACCTG CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCCCCTCTACGTCTTCTCCGAGTTC AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA GAAAGGCCTCTCAGCAGGCTCCAGAGCGATCTTCAGACTCCAGAGTCGAATGAAAAT GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGGAAAACTTCTTGGTGCTCAAAGCAAAG GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGTCCCATCATTGCTGCTGTCAAGGAC GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA CAGGTGGTGGTGGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA AAGGITGCTCGCCTGGACAACATATTCCTGACAACGAATGCACTGGTCTAATGTTGGGGGC AAGGTTGCTCGCCTGGACATATTCCTGACACGATGCACTGGTCTAATGTTGGGGGC TTAAGTGGAATGATTCTTAACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA Traactiggaargarrictraactifraaaggaaacciggcifriccaaagriggarctrictigga CCTCCACACTGGAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA ATAGAACTGGCTGTGCGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT GAGCCACACCTTCCACATGGTGTTAGCCAGAGAGAGGGGGTCAGGGACTCTTCCCTGGTC GAGCCACATCCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC .; 0 Length Indels 6 5 DB Score 2477.8; Pred. No. 0; 0; Mismatches .; 0 99.9%;

GTGGTCTATTCCGGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2100	BC004158 Homo sapiens, putative prostate cancer susceptibility protein, clone MGC:2441 IMAGE:2820640, mRNA, complete cds. BC004158 BC004158 BC004158.1 GI:13278770 MGC. Homo sapiens. Homo sapiens. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mamalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Direct Submission. Institute all Callon (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA INH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-rommail: nh.gov Contact: MGC Project URL: http://mgc.nci.nih.gov Contact: MGC Project URL: http://mgc.nci.nih.gov Contact: MGC Project URL: http://mgc.nci.nih.gov Contact: MGC Project URL: http://mgc.nci.nih.gov Contact: MGC Project URL: http://mgc.nci.nih.gov Contact: MGC Project URL: http://mgc.nci.nih.gov Contact: MGC Project URL: http://mgc.nci.nih.gov Contact: MGC Project URL: http://mgc.nci.nih.gov Contact: MGC Project URL: http://mgc.nci.nih.gov Contact: amadan@systemsbiology.org contact: amadan@systemsbiology.org Contact: amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact: Amadan@systemsbiology.org Contact One distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Contact One was selected for full length sequencing because it This clone was selected for full length sequencing because it Location(Qualifiters Location Contact: Amadan@systemsbiology.org
Db 2041 QY 2041 Db 2101 QY 2161 QY 2221 Db 2221 Db 2281 Db 2341 Db 2401 QY 2401 QY 2461 QY 2461 Db 2461 Db 2461 Db 2451 Db 2451 Db 2451 Db 2451 Db 2451 Db 2521	RESULT 4 BC004158 LOCUS DEFINITION ACCESION VERYWORDS SOURCE SOURCE AUTHORS TITLE JOURNAL REMARK COMMENT FEATURES SOURCE SOURCE AUTHORS TITLE JOURNAL REMARK COMMENT
1020 1080 1080 1140 1200 1200 1320 1320 1380 1440	1500 1500 1560 1620 1680 1740 1800 1860 1920 1920 1980
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TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGCGTG
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ANDGKSITHEGREIJAEELCTPPPDFGAAFVVUECPDESFIQPICENAFFORYGKAD
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ISLLRRTGLEBEQTCLYRHCKARFCGALVHTGGWKVYYSGDTMPCEALLYRMCKDATL
LIHBATLEDGLEBERGTGLYRHGKTAFGTGARGWKYYSGDTMPCRALVRMCKDATL
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KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKV
ARLDNIFLTRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKG
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/tissue type="lung, small cell carcinoma"
/clone_lib="NIH MGC 7"
/lab_host="DH10B-R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2477.8;
Pred. No. 0;
0; Mismatches
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db_xref="LocusID:60528"
db_xref="taxon:9606"
                                                                                                               note="Vector: pOTB7"
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IEBAYRPPAPBYEDETWTVYQIPIHKEQRRGAHQPWGSPRETLSKLSESESNESN
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AVKDGKSITHEGREILABELCTPPDPGAAFVVVECPDESFIQPICENATFQRYGGKAD
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HPDI PPLLTFSPEKREGPTLSVPWYQGDCLLKYQLRPREMORDAIITCNPEEFIIEA
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DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLLNILLQRERAL
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ISSLLAKTOLEBEQTCLVRHKCHAFGCALUHTSGWKVYXSOEDIMPCEALURMGKAATL
LIHBATLEBOGLEBEAVEKTHSTTSQAISVRRMABETIMLNHFSQRYAKUPLESPUFN
EKVGVAFDHWKVCFGDFATMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84103, USA
Location/Qualifiers
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                                                                                                                                                                     A candidate prostate cancer susceptibility gene at chromosome 17p Nat. Genet. 27 (2), 172-180 (2001)
Ghaffari,S., Gupte,J.S., Hu,R., Iliev,D., Janecki,T., Kort,E.N., Laity,K.E., Leavitt,A., Leblanc,G., McArthur-Morrison,J., Pederson,A., Penn,B., Peterson,K.T., Reid,J.E., Richardes,S., Schroeder,M., Smith,R., Snyder,S.C., Swedlund,B., Swensen,J., Thomas,A., Tranchant,M., Woodland,A.M., Labrie,F., Skolnick,M.H., Neuhausen,S., Rommens,J. and Cannon-Albright,L.A.
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llarity 99.4%; Pred. No. 0;
Conservative 0; Mismatches 16;
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1. .2481
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1 (bases 1 to 2908)
Tavtigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Catillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C.,
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                                                                        CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC
                                                                                                                                                                                                          CCCAACCAGCTCAAAGCCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC
                                                                                                                                                                                                                                                                                                                                 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGAATCTCCAGTCCTGCA
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                                       CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC
                                                                                                                                                                                                                                                                                                1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA
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121 CGCACGCGAGAAGAGCGCGGACCGTCGGGGTGCTCCGGCGGCGCCCAAACACCGTGTACCTG 180

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Pan

AUTHORS REFERENCE

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT 5 AF308698 LOCUS

121 COCACACACACACACACACACACACACACACACACACAC	Db 1201 ACCAGTTTCCCCTGTAAGA		Oy 1321 TGCAATCCTGAGGAATTC2	Oy 1381 CAGGAGTACAGGAGGGGGTC	QY 1441 CCAGAAATCATCTTCCTTC	Qy 1501 GCCACACTTGTCAACATAU Db 1501 GCCACACTTGTCAACATAU	Qy 1561 TTTGGGCAGCTGTGCCGTCTCCTTTGGGCAGCTGTGCCGTTTTTGGGCAGCTGTGCCGTTTTGGGCAGCTGTGCCGTT	Qy 1621 GCTGTGTTTGTGTCCCACC		0y 1741 CCCAACCAGCTCAAAGCC 	Qy 1801 CACATCAGTAGATTCCTCTCTCTCTCTCTCTCTCTCTCTC	Qy 1861 GTGGAAAGATTGATCAGT 	Oy 1921 CTGGTGCGGCACTGCAAG	Oy 1981 GTGGTCTATTCCGGGGAC, Db 1981 GTGGTCTATTCCGGGGAC		Qy 2101 ACACACAGCACAACGTCO	Oy 2161 ATGCTGAACCACTTCAGC 	Oy 2221 GAGAAAGTGGGAGTTGCC 	Oy 2281 CCCAAGCTGATTCCCCCA	
2	121 CGCACGCGAGAGAGAGGGGGGGCGTCGGGGGGGGCGCGCGAACACCGTGTGGGGGGGG	181 CAGGIGGIGGCAGCGGGACTCGGGCGCCCGCGCTCTACTCCGAGTTC	241 AACCGGTATCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGACACAAGTTA	301 AAGGTTGCTCTCTGGACAACATATTCCTGACAATGCACGGACGG	361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTGT	421 CCTCCACAACTGGAAAATACCTCGAAGCAATCAAATATTTTTTTT	481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 	541 TACCAGATCCCCATACACAGTGAACAGAGGGGGAAAAGCACCAACCA	601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGCGATCTTCAGACTCCGAGTCAAATGAAAAT	661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGGTCAGGGACTCTTCCCTGGTC	721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGGAAGCAACTTCTTGGTGCTCAAAGCAAAG 721 GTAGCTTTCATCTGTAAGCTTTCACTTAAAGAAAGAAAAATTCTTGGTGCTCAAAGCAAAA	781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCACTCCCATCATTGCTGTGAGGACACTAGTGATGGGCCTCCCATCATTGCTGTTAGGACAGCTGCCATCGCTCCCATCATTGCAACAGCTGCCATGGCTTGGGACAGCTGCCCATGGCTTGGACAGCTGCCATGGCTTGCAACACGCTGCCCATGGCTTGCAACACGCTGCCCATGGCTTGCAA		901 GATCCTGGTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCA	961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCGTGGCTTGGTG	1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGA	1021 GITCACATGGCCCCAGAATCTGTGCTTGTGGACAGGTACCAGCAGTGCAGGGGGGGG	1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCGGACATCTTCCCCCTGCTC	1201 ACCAGTTTCCGCTGTAAGAAGGAGGCCCCACCCTCAGTGGCCCCATGGTTCAGGTGAA	

TGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500 1560 1620 1620 1680 1680 1740 1740 1800 1800 1860 1860 1920 1920 1980 1980 2040 2040 2100 2100 2160 2160 2220 2220 2280 ACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGAAGGAG 2340 rececageaceaceaceaceageagaaaaaaaagaagaaa 1440 SAAGGAGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260 CCTGCACGCAGATCACCACACGGGCTTGCTAAATATCTTGCTG GGCATCTTTGGGAAAGCCCTTTCACCCTTTGCTGGTGGTTGCC CACCATGCCTGCGAGGCTCTGGTCCGGATGGGGAAGATGCC CCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAAC CTTTGACCACATGAAGGTCTGCTTTGGAGACTTTGCAACAATG 3GCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC CTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC TTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT GCATGCGTTTGGCTGTGCTGCTGCACCTCTGGCTGGAAA CCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT CATAGITGAGGGGTGCAGCITCCCAACITCCAGCAGCGTG CCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG CTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC CACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC AGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG CCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT CCAGCGCTATGCCAAGGTCCCCCTTCAGCCCCCAACTTCAGC CTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG SCTCCGTCCCAGGAGGGAGTGCCAGTGCCATTATTACT GCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT AAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA PCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT recchantecerreageagegergagarcrecagrecrech

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Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Direct Submitssion

Bounitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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HPDIFPLLTSFRCKEGPTLSVPMVQGECLLKYQLRPRREWQRDAIITCNPEEFIVEAL
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                          2341 CGCAGGAGAAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCGCCTCCTGTCCAGGGAGCTGGCA
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Homo sapiens cDNA FLJ10530 fis, clone NT2RP2000985.
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oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell line:NT2
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Homo sapiens
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QLPNFQQSVQEYRRSAQDGPAPAEKRSQYPEIIFLGTGSAIPMKIRNVSATLVNISPD
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Pred. No. 0;
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llarity 99.7%;
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APVALVVHMAPESVLVDSRYQWMEREGPDTQHLVLABNCASVHNLRSHKIGTQLNLI
HEDIFPLITZPECKKEGPTLSVPMYQSECLLKYQLRPREMORDAIITCNPEEFIVEA
LQLPNFQOSVOEYRRSWQDVPRAVQSECLLKYQLRPREMORDAIITCNPEEFIVEA
LQLPNFQOSVOEYRRSWQDVPRAVQSECLLKYQPTBITFLGTGSAIPMKIRNVSATLVNISP
DYSLLLDCGEGFFGQLCRHYGDQVBVVLGTLAAVFVSHLHADHHTGLLNILLQFREQAL
ASLGKPLHPLLVVAPSQLKAWLQQYHNQCQFVLHHISMIPAGNTACCLQFGAEISSPAVEL
LIHEATLEDGLEEFQTCLVRTCKHAFGCALVHTSGWKVVYSGDTMPCEALLYRMCKDATL
LIHEATLEDGLEEFATELVRTGKAFGCALVHTSGALVKVVPLFSPNFN
EKVGVAFDHMKVCFGDFFTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSGE
LAGGLEDGEPQQKRAHTEBPQAKKVRAQ"
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/db_xref="G1:10946489"
/db_xref="G1:10946489"
/translation="WMALCSLIRSAAGRTMSQGRTISQAPARRERPREDPLRHIRRTRE
/translation="WMALCSLIRSAAGRTWSGGRTISQAPARRERPREDFRHIRRTRE
VREDSGGGGGDPTVYLQVYAGSRDSGAALVYFSEFNRYLFNGGGGVQRLMQEHKLKV
VRLDNIFLTRHWWSWVGGLSGMILTHKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKG
IELAVRPHSAPESYEDETWTVYQIPIHSEQRRGRHQPWQSPERPLSRLSPERSGDSESN
ENEPHLPHGPYGQRRGVRDSSLVVAFICKLHLKRGNFLVLKAKEMGLPVGTAAIAPIIA
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Unpublished
J (bases 1 to 2893)
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Javigan, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A.,
Camp, N.J., Carillo, A.R., Chen, Y., Dayanath, P., Desrochers, M.,
Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S.,
Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K.E.,
Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B.,
Peterson, K.T., Reid, J.B., Richards, S., Schroeder, M., Smith, R.,
Woodland, A.-M., Labrie, F., Swensen, J., Thomas, A., Tranchant, M.,
and Cannon-Albright, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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    forganism="Gorilla gorilla"
    db_xref="taxon:9593"
    2893

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Submitted (27-SEP-2000) Myriad
Lake City, UT 84103, USA
Location/Qualifiers
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Matches 2457; Conservative
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1411 CCALANTITATIONALANA AND ASSOCIATION A

RESULT

Sisogal, T. and Yanamoto, J.

Sisogal, T. and Yanamoto, J.

Sisogal, T. and Yanamoto, J.

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

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(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB. AK094687

1907 bp mRNA linear PRI 15-JUL-2002 Homo sapiens cDNA FLJ37368 fis, clone BRAMY2024530, highly similar to Homo sapiens prostate cancer susceptibility protein HPC2/ELAC2 Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Saco, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. CGCACGCGAGAGAGCGCGGACCGTCGGGGTGCTCCGGCGCCCCAAACACCGTGTACCTG 180 cecaceceasasas de constante de CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCTCTACGTCTTCTCCGAGTTC 240 59 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 118 61 ACCATATCGCAGGCACCCGCCGCGGCGGCGGCCGCCAAGGACCCGCTGCGGCACCTG 120 241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300 ------GGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 301 1 ATGTGGGCGCTTTGCTCGCTGCGGTCCGCGGCCGGACGCACGTGTCGCAGGGACGC 60 57; 94.7%; Score 2349; DB 9; Length 2907; 97.5%; Pred. No. 0; Live 0; Mismatches 5; Indels 57; oligo capping; fis (full insert sequence). Homo sapiens awygdala cDNA to mRNA, clone_lib:BRAMY2 clone:BRAMY2024530. /tissue type="amygdala" /clone lib="BRAMY2" /note="cloning vector: pME18SFL3" 788 c 839 g 584 t /organism="Homo sapiens" /db_xref="taxon:9606" /clone="BRAMY2024530" AK094687.1 GI:21753794 (bases 1 to 2907) Local Similarity 97.5 hes 2419; Conservative Homo sapiens AK094687 v Match ES LION TNDC 179 181 NO. NO. AAL ACE ORS 121 269 ACE ORS 염

CACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGGGGGCACG TGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG GGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 3GTCTATTCCGGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC ACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT GCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC CAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGCGGCCGCCTCTCTCCCAGGGAGCTGGCA CACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGAGGGCACA CAACCAGCTCAAAGCCTGGCTCCAGCAGTACCAGAACCAGTGCCAGGAGGTCCTGCAC SGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT SCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCCAACTTCAGC CAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGCGCCCTCCTGTCCAGGGAAGCTGGCA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (6-7012) Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics@hri.co.jp, Tel:81-438-52-3986) Winistry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA full insert sequencing: Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; Incation/Qualifiers
                                                                           AK094333 2734 bp mRNA linear PRI 15-JUL-2002 Homo sapiens CDNA FLJ37014 fis, clone BRACE2010203, highly similar to Homo sapiens prostate cancer susceptibility protein HPC2/ELAC2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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oligo capping; fis (full insert sequence).
Homo sapiens cerebellum cDNA to mRNA, clone_lib:BRACE2 clone:BRACE2010203.
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/clone lib="BRACE2"
/note="cloning vector: pMI 708 c 724 g 631
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/db_xref="taxon:9606"
/clone="BRACE2010203"
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2462 AAGAAGGTCAGAGCCCAGTGA 2482
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TTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTGGTTCACATGGCCCCAG
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                                                                                                                                                                                                                      AGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTC
                                                                                                                                                                                                                                                                                                                                                                                                         AAACCCAGCTCAACCTCATCCACCGGACATCTTCCCCCTGCTCACCAGTTTCCGCTGTA
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                                                                                              AGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTC
                                                                                                                                                                                                                                                                                                                                               AAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTCACCAGTTTCCGCTGTA
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/note="cloning vector: pME18SFL3"
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Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dái, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@ins.u-tokyo.ac.jp, Tel:81-3-5449-5286,
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AK074244.1 GI:18676795
Oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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AUTHORS REFERENCE

TITLE JOURNAL

			and Cannon-Albright, L.A. Direct Submission Submitted (26-DEC-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt Lake City, UT 84103, USA Sequence update by submitter On Dec 26, 2000 this sequence version replaced gi:10946492. Location/Qualifiers 12712 / Organism="Mus musculus" / db xref="taxon:10090" / dev_stage="fetus" 152510 / note="similar to Homo sapiens HPC2/ELAC2"	/codon_start=1 /product="BLAC2" /protein id="AdG24918.27 /protein id="AdG24918.27 /translation="WMALRSILK GGPWTVYLQVVAAGGRDGAGALN TRHIMSNVGGLCGMILTLKETGI SAPEYKDETMTVYQVPIHSERR DSSAGANKRAMEDPSLVAFVV GKSITYEGREIAAEELCTPPPPP GKSITYEGREIAAEECTPPPPP GKSITYEGREIAAEECTPPPPP GKSITYEGREIAAEECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPPP GKSITYEGREIAAECTPPPP GKSITYEGREIAAECTPPPP GKSITYEGREIAAECTPPPP GKSITYEGREIAAECTPPPP GKSITYEGREIAAECTPPP GKSITYEGREIAAECTPPP GKSITYEGREIAAECTPP GKSITYEGREIAAECTPP GKSITYEGREIAAECTPP GKSITYEGREIAAECTP GKSITYEGREIAAECTP GKSITYEGREIAAECTP GKSITYEGREIAAECTP GKSITYEGREIAAECT GKSITYEGRE
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	1141 GGAAGAGTTTCAGACCTGTCTGGTGCGCACTGCATGCGTTTGGCTGTGGTTTGGCTGGTTTGGCTGTGGTTTGGCTGGTGG	DD 1321 AGAGGAAGCAGTGGAAAAAGACACACACACCACCAAACCTTCAACCATCAGCGTGGGGATGCG 1380 OY 2142 GATGAACGCGGAGTTCATTATGCTGAACCACTTCAGCCAGC	0y 2322 CATCGAGGAGTATGGAGGAGGAGAGGTGCGGGAGGTGCGGGCGCCCT 2381 Db 1561 CATCGAGGAGTGGAGAGGAGAGAGGGGGGGGCGCGCGGCGCGCGC	AF308696 AF308696 LOCUS BEFINITION WE musculus ELAC2 mRNA, complete cds. ACCESSION AF308696.2 GI:11992378 KEYWORDS ONGANISM WE musculus. ONGANISM ATTHORS BLAZDAN AUTHORS A

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S Isogal, T. and Yamamoto, J.

L Submitted (104-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0912, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA ibrary construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation; HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                     AKU94012 2793 bp mRNA linear PRI 15-JUL-2002 Homo sapiens cDNA FLJ36693 fis, clone UTERU2008901, highly similar to Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamateu, A., 18hii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Yamashita, M., Marzakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                    2325
                                                                                                                                                                     2385
                                                                                                                                                                                                    2387
                                                                                                                                                                                                                                                     2388 ACC---CAGCAGGCAGACAGCCCAGAGGACAGAACCCCAACAGAAGCGGGCCCACACA 2444
                                                                                                                                                                                            2328 GAAGAGATGGTGGAAACGCAGGGAGAAAGAGGGAGAACGAGCTACGGCTGCTGCGAGCAGCCTCCTG
AATGCGGGGTTCATCATGCTGAACCACTTCAGTCAGCGGTACGCCAAGATCCCCCTTTTTC
                                                       GACTITICCAACAATGCCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATC
                                                                                                                               2268 GACTICCCGACAGGIGCCCAAGCIGATICCCCCACTGAAGGCCCCTGTTTGCAGGTGACATT
                                                                                                                                                                GAGGAGATGGAGGAGCGCAGGGAGAAAGCGGGAGCTGCGGCAGGTGCGGGGGGGCCCTCCTG
                                                                                                                                                                                                                                  2386 TCCAGGGAGCTGGCAGGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACA
                                AGCCCCAACTTCAGCGAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insert sequence).
to mRNA, clone_lib:UTERU2
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/db_xref="taxon:9606"
/clone="UTERU2008901"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="uterus"
/clone lib="UTERU2"
/note="cloning vector:
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1. .2793
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AK094012
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AUTHORS
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JOURNAL
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Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.
AC005277
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCCTGTCCAGGGAGCTGGAGGGGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGC 2325
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                                                                                                                                                                                                                                                                                      1606 TCACCCTTGCTGGTGGTTGCCCCCCAACCAGCTCAAAGCCTGGCTCCAGCACCACAAA
                                                                                                                                                                                                                                                                                                                                                                                                             CCAGTGCCAGGAGGTCCTGCACCACCACCATCAGTATCATTCCTGCCAAATGCCTTCAGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTGAGATCTCCAGTCCTGCAGTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGA
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                                                                                                                                      GGGCTTGCCAAGTATCTTGCTGCAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCT
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                     Length 2793;
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                  Score 823; DB 9; Le
Pred. No. 7.1e-181;
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100.0%; Pred. No. '...
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                                                                               Conservative
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Homo sapiens
                                             Similarity
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complement(19638..19896)
/rpt_family="MIR"
complement(19971..20260)
/rpt_family="LiME3A"
20263..20552
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/rpc_family="L2"
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/rpt_family="MER39"
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/rpt_family="MER91A"
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complement(20553. .20816)
/rpt_family="L1ME3A"
complement(20821. .21069)
                                                                                                                                                                                                                                                                         complement (6411. .6494)
/rpt_family="MER5A"
6830. .7013
                                                                                       family="MER89"
ement (Apr
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ement(For
                                /rpt_family="(TAAA)n"
complement (4328. .4608)
/rpt_family="AluSx"
                                                                                                                                complement (4896...5186)
/rpt_family="AluSp"
5219...5479
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7721. .8032
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8039. .8333
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7319. .7581

    14153
    family="(CA)n"

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1014. .7318
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9431. .9460
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.8271. .18311
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family="L2"
            complement (4282.
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                                                 CEE 2 (bases 1 to 118788)

Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Baker, J., Baldwin, A., Castle, A., Cerny, J., Cooke, P., Depayre, E., Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Mardula, N., Mozwan, P., McGurk, A., McKernan, K., Maddrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

25 S (bases 1 to 118788)

26 Birren, B. Fesman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Botten, Castle, A., Cerly, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Fitzlugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Gersigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Mellarim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Nioff, M., O'Connor, T., Pavlin, B., Peterson, K., Ribey, R., Roberts, D., Rossello, R., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 01 ULS Lips this sequence version replaced gi:3335015.
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Only the first 118.8 kilobases of this clone are being submitted.
The remainder overlaps accession number AC005274 (WICGR project
Birren, B., Fasman, K., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone hRPK.597_M_12
Unpublished
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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clone lb="RPCI-11 human BAC library"
75. 884
rpt_family="MIR"
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/organism="Homo sapiens"
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/chromosome="17"
/map="17"
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1822. .4007
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/rpt_family="L2"
complement(4015.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

B. 1 (bases 1 to 740)

S. Tattigian, S. V., Simard, J., Teng, D. H.F., Baumgard, M., Beck, A., Cartigian, S. V., Simard, J., Teng, D. H.F., Baumgard, M., Beck, A., Camp, N. J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J. M., Frank, D., Frye, C., Ghaffari, S., Gupte, J. S., H., R., Illev, D., Janecki, T., Kort, E. N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S. C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
A strong candidate prostate cancer susceptibility gene at
                                                                                                              Homo sapiens

Bukaryota; Metacas; Chordata; Craniata; Vertebrata; Euteleostomi;

Bumanlia; Eutheria;

Toases 1 to 679)

Rutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matuschko, O.V.,

Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I.,

Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.

Not! flanking sequences: a tool for gene discovery and verification of the human genome

Noteleic Acids Res. 30 (14), 3163-3170 (2002)
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Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
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Homo sapiens putative prostate cancer susceptibility protein HPCZ/ELAC2 gene, exon 17 and partial cds.
Homo sapiens genomic sequence surrounding NotI site, clone NL6-B020C.
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Pred. No. 1.1e-25;
0; Mismatches 7;
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/db_xref="taxon:9606"
/clone="NL6-B020C"
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95.8%;
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Zabarovsky, E.R.
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Best Local Similarity 95.8
Matches 161; Conservative
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Best Local Similarity 97.7%; Pred. No. 1.1e-46;
Matches 251; Conservative 0; Mismatches 6
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          /rpc_family="(TAAA)"

/rpc_family="(TAAA)"

complement (21101. .21338)

/rpc_family="AluSx"

complement (21348. .21598)

/rpc_family="L1M4"

21799. .22104
                                                                                                                                                                                                                                                /.c._cent.p="Atlusq"
24852. .25199
/rpt_family="L2"
complement(25697. .25985)
/rpt_family="MLTID"
25816. .25895
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'8034. .28197
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:6991. .2729A
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complement (26576. .26781)
rpt family="MER6B"
complement (26912. .26990)
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/rpt family="purine-rich"
complement (26122. .26291)
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:6456. .26480
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28920. .29005
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29140. .29233
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complement(27291. .
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                                                                                                                                                            rpt_family="AluJo"
2151. .22562
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S Tavidjan,S.V., Simard,J., Teng,D.H.F., Baumgard,M., Beck,A.,
Camp,N.J., Carillo,A.R., Chen,Y., Dayananth,P., Desrochers,M.,
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Direct Submission
L. Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84108, USA
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5.9%; Score 146.2; DB 9; Length 740;
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Sequence 223, App
Sequence 225, App
Sequence 221, App
Sequence 210, App
                                                                                                             May 17, 2003, 15:56:54 ; Search time 139.603 Seconds (without alignments) 5450.193 Million cell updates/sec
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GenCore version 5.1.5
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241 AACCGGTATCTCTTCAACTGTGGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA	Db 241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300 Oy 301 AAGGTTGCCTGGACAACATATCCTGACACAATGCACGGTCTAATGTTGGGGGC 360 Db 301 AAGGTTGCTCCTGGACAACATTTCCTGACAATGCACTGTTTAATGTTGAGTGAG	361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTACTTTCTGAA 361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTACTTTCTGA 361 TTAAGTGGAATGATTTTAATTTAAAGGAAACGGGCTTCCAAAGTGTACTTTCTTGA	CCTCCACAACTGGAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 	Oy 481 ATAGAACTGGCTGTGCGGCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540	Oy 541 TACCAGATCCCCATACACAGTGAACAGAGGGAAAGCACCAACCA	601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 601 GAAAGGCCTCTCAGCAGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT	Qy 661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720 Db 661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720	Oy 721 GTAGCTTTCATCTAAAGCTTCACTTAAAGAGAGAAACTTCTTGGTGCTCAAAGCAAAG 780	781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGTCCCATCATTGCTGCTGTCAAGGACAGTGGCTGCTGTCAAGGACAGTGGGACAGCTGCCATCGCTCCCATTGCTGCTGTCAAGGACAGTTGGGACAGCTGCCATCGCTCCCATCGTTGCTGCTGTCAAGGAC	Qy 841 GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900 Db 841 GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900	Qy 901 GATCCTGGTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCA	Qy 961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCGGTGGCCTTGGTG 1020 Db 961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020	Qy 1021 GTTCACATGGCCCCAGCATCTGTGGACAGCAGCAGCAGCAGCAGCAGGAGGGGGGGG	OY 1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140	1141 GGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCGGACATCTTCCCCCTGCTC	Qy 1201 ACCAGTTTCCGCTGTAAGAAGAGGCCCCACCCTCAGTGCCCATGGTTCAGGGTGAA 1260 Db 1201 ACCAGTTTCCGCTGTAAGAAGAGGCCCCACCTCAGTGTGCCCATGGTTCAGGGTGAA 1260	Oy 1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGAGGGAGG	OY 1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGGGGTG 1380
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APPLICANT: Tavidaian, Sean V.
APPLICANT: Tavidaian, Sean V.
APPLICANT: Tavidad H.F.
APPLICANT: Romands. Joacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome I/P-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2958
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COTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-564-805-3
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100.0%; Score 2481;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches
                                                                                                ; Sequence 3, Application US/09564805; Patent No. 6333403; GENERAL INFORMATION:
                                   2461 AAGAAGGTCAGAGCCCAGTGA
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ORGANISM: Homo sapiens
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Sequence 223, Application US/09564805 Patent No. 6333403 GENERAL INFORMATION:

RESULT 3 US-09-564-805-223

APPLICANT: Tavtigian, Sean V. APPLICANT: Teng, David H.F. APPLICANT: Simard, Jacques

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APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPERENCE: 2318-28
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NOS: 240
SEQ ID NO 223
LIENGTH: 2908
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Pred. No. 0;
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Best Local Similarity 99.4%;
Matches 2465; Conservative
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US-09-564-805-223
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0	RESULT 4 US-09-564 805-225 JS Sequence 225, Application US/09564805 Sequence 225, Application US/09564805 Patent No. 6333403 GENERAL INFORMATION: APPLICANT: Taviglan, Sean V. APPLICANT: Rommens. Johanna M. APPLICANT: Simard, Jacques APPLICANT: Sommens. Johanna M. APPLICANT: Rommens. Johanna M. APPLICANT: Myriad Genetics, Inc. TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes FILE REPERENCE: 2318-258 CURRENT FILING DATE: 200-05-05 FRIOR APPLICATION NUMBER: US 60/107,468 FRIOR APPLICATION NUMBER: US 60/107,468 FRIOR APPLICATION NUMBER: US 60/107,468 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR APPLICATION NUMBER: 09/434,382
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Pred. No. 0;
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99.0%;
                                                               Best Local Similarity 99.0
Matches 2457; Conservative
gorilla
                 ; NAME/KEY: CDS
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US-09-564-805-225
ORGANISM: Gorilla FEATURE:
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APPLICANT: Tavidian, Sean V.
APPLICANT: Simard, Joaques
APPLICANT: Simard, Joaques
APPLICANT: Simard, Joaques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 221
LENGTH: 2470
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Patent No. 6333403
GENERAL INFORMATION:
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; NAME/KEY: CDS
; LOCATION: (1).
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APPLICANT: Tavitidan, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Romenens, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
                     2299 GAACGCAGGAGAAAAAGGGGAGCTACGGTGCGAGCAGCCCTCCTGACC---CAGCAG 2355
2356 GCAGACAGCCCAGAGGACAGAGAACCCCAACAGAAGCGGGCCCACAGAATGAACCACA 2414
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Pred. No. 2.1e-57;
0; Mismatches 6;
                                                                                                                                                                                         US-09-564-805-210
; Sequence 210, Application US/09564805
; Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/09564805; Patent No. 6333403
Patent No. 6333403
GENERAL INFORMATION:
APPLICANT: Teng, David H.F.,
APPLICANT: Simard, Jacques,
APPLICANT: Rommens, Johanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%;
ilarity 97.7%;
Conservative (
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 251; Conserv
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (51)
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APPLICANT: Commens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
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Matches 245; Conservative
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CCATION: (51)..(295)

CTHER INFORMATION: exon 1

US-09-564-885-4
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
          Tavtigian,
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR PILING DATE: 1998-11.06
PRIOR FILING DATE: 1998-11.06
PRIOR FILING DATE: 1998-11.05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCCAAACACCGTGTACCTG
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Patent No. 6333403
GENERAL INFORMATION:
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Matches 251; Conservative
                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                        LENGTH: 26664
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US-09-564-805-4
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US-09-564-805-16
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Now Genee and a Paralog and Orthologous Genes
CURRENT APPLICATION UNMERR: US/09/564,805
CURRENT APPLICATION UNMERR: US 60/107,468
PRIOR APPLICATION UNMERR: US 60/107,468
PRIOR APPLICATION UNMERR: US 60/107,468
PRIOR APPLICATION UNMERR: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AGTTAAAGGTTGCTCGCCTGGACAACATATTCCTGACAAGGAATGCACTGGTCTAATGTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AGTICAACCGGIAICTCTICAACTGTGGAGAAGGCGTICAGAGACTCATGCAGGAGCACA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AGTTCAACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTTAAAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTG 355
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                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                               GGGGCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTAC 412
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                                                                                                                                                                                                                                                                                                                                                176 ACCTGCAGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCG
                                                                                                                                                                                                                                               Length 238;
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                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                 9.6%; Score 237; DB 4; I 100.0%; Pred. No. 1.1e-54; tive 0; Mismatches 0;
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100.0%; Pred. No. 5.1e-52;
iive 0; Mismatches 0;
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SEGTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 315
LENGTH: 238
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Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
; LOCATION: (1)...(228)
; OTHER INFORMATION: exon 24;
; NAME/KEY: polyA_signal
; LOCATION: (546)...(641)
US-09-564-805-27
                                                                                                                                                                                                                                                                        Best Local Similarity 100.0
Matches 237; Conservative
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Best Local Similarity 100.
Matches 228; Conservative
                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-315
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US-09-564-805-27
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Best Local
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US-09-564-805-26

Sequence 26 Application US/09564805

Sequence 26 Application US/09564805

Sequence 26 Application US/09564805

Sequence 26 Application

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Simard, Jacques

APPLICANT: Simard, Johanna M.

APPLICANT: Rommens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT FILING DATE: 2000-05-05

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 26

SEQ ID NO 26

LENGTH: 145
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Patent No. 6333403
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simach, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
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61 GCTGGCGACATCGAGGAGATGGAGGAGCGCAGGAGAAGCGGGAGCTGCGGCAGGTGCGG 120
                                                                                                                            121 ecececercereredecadecadecadecedecedecadedarecedadeceredadad 180
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                                                                 2374 GCGGCCCTCCTGTCCAGGGAGCTGGCAGGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAG
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100.0%; Pred. No. 6e-30; .
tive 0; Mismatches 0; Indels
                                                                                                                                                                                              2434 CGGCCCACACAGAGGAGCCACAGGCCAAGAAGGTCAGAGCCCCAGTGA 2481
                                                                                                                                                                                                                                  181 CGGGCCCACACAGAGGAGCCACAGGCCAAGAAGGTCAGAGCCCAGTGA 228
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Best Local Similarity 100.0
Matches 145; Conservative
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; OTHER INFORMATION: exon 23
US-09-564-805-26
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GENERAL INFORMATION:
APPLICANT: Tavigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
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                                               TTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTGTTTGTGTCCCCACCT 1640
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100.0%; Pred. No. 1.7e-23;
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12-09-564-805-24
Sequence 24, Application US/09564805
Patent No. 6333403
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                                                                                                                                                                             1641 GCACGCAGATCACCACACG 1659
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Best Local Similarity 100.0
Matches 121; Conservative
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LOCATION: (1)...(121)

COTHER INFORMATION: exon 21

US-09-564-805-24
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US-09~564-805-10
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
ITILE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: US/41,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 139
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100.0%; Pred. No. 2.5e-28;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.6%; Score 139; DB 4; 3 100.0%; Pred. No. 2.5e-28; iive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 16
LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 20, Application US/09564805; Patent No. 6333403
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Best Local Similarity 100.0
Matches 139; Conservative
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US-09-564-805-20
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

LOCATION: (1)..(139)

CTHER INFORMATION: exon 13

US-09-564-805-16
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Matches 139; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1)...(139)
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ORGANISM: Homo sapiens
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CORNERAL INFORMATION:

APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Saques
APPLICANT: Tavtigian, Saques
APPLICANT: Simmard, Joaques
APPLICANT: Rommens, Joaques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 179-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 179-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT APPLICATION NUMBER: US/054,805
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO 1
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US-09-988-687-10

US-09-988-687-20

US-09-988-687-20

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100.0%; Score 2481;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09988626 Publication No. US20030044959A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
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Sequence 223, Appli
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Sequence 225, App
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NWW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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                  GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      nucleic search, using sw model
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qq	121	GCACGCGAGAAAGCGCGGACGTCGGGGTGCTCCGGCGCCCAAACACCGTGTATTTTTTTT	a è	4 -
ò	181	CAGGIGGCAGCGGGAACCGGGACTCGGGCCCCGCTCTTCTCCGAGTTC 240	3 E	1261 1661
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ò	-	CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
qq	H	CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT
yo da		GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA
6	H	TTTGGGCGCCCTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCTGGGCT
Ĭ	н	TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGCTGGGGCTCCTGGGCTCCTGGGCT
ò	Н	GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG
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ò	Ä	CAGAGAGAACGCGCTTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
q	H	CAGAGAGAACGCCCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
ò	H	CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
qq	Н	cccaaccacrtcaaagccrccaccagcagraccacaaccagraccaggaggrccracac 1800
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ò	7	ACCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
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qq	2	ACACACAGACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
ò	2	ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCCAACTTCAGC 2220
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ò	7	GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
qq	73	GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280

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CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA
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Publication No. US20030045704A1

GENERAL INPORMATION:

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Jacques

APPLICANT: Sinard, Jacques

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,687

CURRENT APPLICATION NUMBER: 09/564,805

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: Patentin Ver. 2.0

LEAST SEQ ID NO S. 240

SEQ ID NO 1.
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR APPLICATION NUMBER: 09/544,805
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 3: SEQ ID NOS: 220
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OTHER INFORMATION: coding sequence as in SEQ ID
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iive 0; Mismatches
                                                                                                                                            Sequence 3, Application US/09988626; Publication No. US20030044959A1; GENERAL INFORMATION:
   2461 AAGAAGGTCAGAGCCCAGTGA 2481
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Db 1611 TTTGGGCAGC	Qy 1621 GCTGTGTTTG Db 1671 GCTGTGTTTG	Oy 1681 CAGAGAACC 	Qy 1741 CCCAACCAGC 	Qy 1801 Db 1851	1861	1921	1981 G 2031 G	2091	0y 2101 ACACAGAGCA Db 2151 ACACAGAGCA	Qy 2161 ATGCTGAACG Db 2211 ATGCTGAACG	Oy 2221 GAGAAGTGG 	2281	Oy 2341 CGCAGGAGAI Db 2391 CGCAGGGAGAI	Oy 2401 GGCGGCCTGG. Db 2451 GGCGGCCTGG.	Oy 2461 AAGAAGGTCA(Db 2511 AAGAAGGTCA	RESULT 4 US-09-988-687-3 ; Sequence 3, Applica	; PUDIICACION NO. US. ; GENERAL INFORMATION ; APPLICANT: Tavtig, ; APPLICANT: Teng,	; APPLICANT: Sımarr; ; APPLICANT: Rommer ; APPLICANT: Myriad
	541 TACCAGATCCCATACACAGTGAACAGAGGGAAAGCACCAACGATGGCAGAGTCCA 600 	601 GAAAGGCCTCTCAGGAGCTCAGAGCGATCTTCAGACTCCGAGTCGAAAAAT 660 	661 GAGCCACACCTTCCACATGGTGTTAGCCAGACAAGAGGGGGTCAGGGACTCTTCCCTGGTC	721 GTAGCTTTCATCTGTAAAGCTTCACTTAAAGAGAAACTTCTTGGTGCTCAAAGCAAAG	781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840	/ 841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900 	901 GATCCTGGTGCTGCTGTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCA	/ 961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020	/ 1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGGGATGGAGAGG 1080 	1081 TTTGGGCCTGACCCGGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140	1141	1201 ACCAGITICCGCIGIAAGAAGGAGGCCCCACCCICAGIGIGCCCAIGGITCAGGIGAA 1260 	/ 1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGAGGGAGGGAGG	1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGGTG 1380 	/ 1381 CAGGAGTACAGGAGGAGGCCCAGCCCCAGCCCCAGCAGAAAAGAAGTCAGTAC 1440 	/ 1441 CCAGAAATGATCTTCCTTGGAAGAGGTCTGCCATCCGGATGAAGATTGGAAATGTCAGT 1500 	/ 1501 GCCACACTIGICAACATAAGCCCGGACACGICICIGCTACIGGACIGIGGIGAGGGCACA 1560 	/ 1561 TTTGGGCAGCTGTGCCGTTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
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qq	1611	TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1670
è	v	168
2 d	9	GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGCTTGCCAAGTATCTTGCTG 1730
ò	1681	CAGAGAGAACGCGCCTTGGCAFCTTGGGAAAGCCGCTTCACCCTTTGCTGCTGGTTGCC 1740
ДQ	1731	179
ò	1741	CCCAACCAGCTCAAAGCCTGCCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
Dp	1791	CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTTGCAC 1850
ò	1801	CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGCTGAGATCTCCAGTCCTGCA 1860
qq	1851	CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1910
ò	1861	GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
qq	1911	GIGGAAAGAIIGAICAGIICGCIGIIGCGAACAIGIGAIIIGGAAGAGIIICAGACCIGI 1970
ò	92	98
Д	1971	CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACCCTCTGGCTGG
ò	1981	04
qq	2031	GIGGICTATICCGGGGACACCAIGCCCIGCGAGGCICIGGICCGGAIGGGGAAAGAIGCC 2090
ò	2041	ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAG 2100
gg	2091	ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2150
ò	2101	ACACACAGCACAACGTCCCAAGCCATCAGCGGGGGATGCGGGATGAACGCGGAGTTCATT 2160
QQ	2151	ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2210
ò	2161	ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCCAACTTCAGC 2220
Dp	2211	ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCCAACTTCAGC 2270
ò	2221	GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGAGTTTCCAACAATG 2280
Db	2271	GAGAAAGTGGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2330
ò	2281	CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
g	2331	CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATGAGGAGAAGGAGAG 2390
δ	2341	CGCAGGGAGAAAGCGGGAAGCTGCGGCAGGTGCGGGCGCCCTCCTGTCCAGGAGCTGGCA 2400
g	2391	CGCAGGGAAAAGCGGGAGCTGCGGCAGCTGCGGCCGCCCTCCTTGTTTTTTTT
ò	2401	GGCGGCCTGGAGGATGGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
q	2451	GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAGCGGGCCCACACAGAGGAGCCACACAGGCC 2510
δ	2461	AAGAAGGTCAGAGCCCAGTGA 2481
qq	2511	AAGAAGGTCAGAGGG 2531
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Sean V.
Ig, David H.F.
Arad, Jacques
Arad, Johanna M.

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TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/64,805
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2958
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LOCATION: (51). (2531)
OTHER INFORMATION: coding sequence as in SEQ ID NO:1
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ORGANISM: Homo sapiens
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Matches 2481;
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; LENGTH: 2908

; TYPE: DNA

; ORCANISM: Pan troglodytes

; FEATURE:

; NAMEX/KEY: CDS

; LOCATION: (1)..(2478)

US-09-988-626-223
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Sequence 223, Application US/09988626

Publication No. US20030044959A1

GENERAL INFORMATION:

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Romens, Johanna M.

APPLICANT: Romens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,626

CURRENT FILING DATE: 2001-01-20

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR APPLICATION NUMBER: 09/434,382

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PatentIn Ver. 2.0
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Query Match
99.0%; Score 2455.4;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2465; Conservative 0; Mismatches
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y applicant: Tergy David H.F.
APPLICANT: Tergy David H.F.
APPLICANT: Tergy David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: US 60/107,468
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241 AACCGGTATCTCTTCAACTGTGGAGAAGCGTTCAGAGACTCATGCAGGAGCACAAGTTA [29y 421 CCTCCACAACTGGAAAAATTCTGGTCCATTGAAAGGA 480 11	541 601 601 661 721 721 721 721 721 721 721 721 721 72	
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Db 2401 GGCGGCCTGGAGGATGCGGAGCCTCAGCAGAAACGGCCCACACAGAGGCCCACAGGCC 2460 Qy 2461 AAGAAGCTCAGAGCCCAGTGA 2481 Db 2461 AAGAAGCTCAGAGCCCAGTGA 2481 RESULT US-09-988-687-25 Sequence 225. Application US/09988687 Sequence 225. Application US/09988687 Sequence 225. Application US/09988687 Sequence 225. Application US/09988687 Sequence 225. Application US/09988687 Sequence 225. Application US/09988687 Sequence 225. Application US/09988687 Sequence 225. Application US/09988687 Sequence 225. Application US/09988687 Sequence 225. Application US/09988687 SepticANT: Transp. Data US-05-05-05-05-05-05-05-05-05-05-05-05-05-	Query Match 98.5%; Score 2442.6; DB 9; Length 2892; Best Local Similarity 99.0%; Pred. No. 0; Matches 2457; Conservative 0; Misantches 24; Indels 0; Gaps 0; ATGTGGGCGCTTTGCTCGCTGCTGCGGCCGGGCGGGCGCGCATGTCGCAGGGACGC 60 Db
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RESULT 9
US-09-988-626-221
S. Sequence 221, Application US/09988626
Publication No. US20030044959A1
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.

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APPLICANT: Teng, David H.F.

APPLICANT: Simard, Jacques
APPLICANT: Somenes, Johanna M.
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Cancer 17p-Linked Prostate Cancer Susceptibility
FILE REPERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2000-05-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOGTWARE: PARCHIN Ver. 2.0
SEQ ID NO 221
LENGTH: 2470

"UNDER OF SEQ ID NOS: 240
SEQ ID NO 221
LENGTH: 2470
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                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mus musculus
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; LOCATION: (1)
US-09-988-626-221
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GENERAL INFURANTION:
GENERAL INFURANTION:
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Johanna M.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
FILE REFERENCE: 218-258
CURRENT APPLICATION NUMBER: US/09/988,687
FILE REFERENCE: 2000-05-05
FRIOR APPLICATION NUMBER: US 60/107,468
FRIOR FILING DATE: 1999-11-05
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US-09-988-687-221
Sequence 221, Application US/0998687
Publication No. US20030045704A1
GENERAL INFORMATION:
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ORGANISM: Mus musculus
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Pred. No. 0;
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Conservative
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Best Local Similarity
Matches 1958; Conserv
; NAME/KEY: CDS
; LOCATION: (1).
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Sequence 2039, Application US/09833381

Fatent No. US20020132090A1

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs
FILE REFERENCE: S800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT PILING DATE: 2001-04-11

PRIOR APPLICATION UNMER: 2001-04-11

PRIOR APPLICATION UNMER: 2000-02-9

NUMBER OF SCO ID NOS: 2050-29

NUMBER OF SEQ ID NOS: 2050-29

SSOTUMARE: FRATSEQ for Windows Version 3.0

LENGTH: 783
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Pred. No. 2e-220;
0; Mismatches 10; Indels 3;
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// LOCATION: (1)...(783)

// OTHER INFORMATION: n = A,T,C or

US-09-833-881-2039
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Best Local Similarity 98.3%;
Matches 772; Conservative 0
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US-09-833-381-2039
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                                                                                                                 CTTCGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCGGACATCTTCCCCCTG
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                                                        ACACGAATGCACTGGTCTAATGTTGGGGGCTTAAGTGGAATGATTCTTACTTTAAAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8996, Application US/09918995
| Publication World US20030073623A1
| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
| TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
| FILE REFERENCE: 20411-756
| CURRENT APPLICATION NUMBER: US/09/918,995
| CURRENT FILING DATE: 2001-07-30
| PRIOR APPLICATION NUMBER: US/09/225,076
| PRIOR PLING DATE: 1999-01-20
| NUMBER OF SEQ ID NOS: 38054
| SEC ID NO 8996
                                                                                                                                                                                                                                                                                    CCAGAATACGAGGATGAAACCATGACAGTTTACCAGATCCCCATACACAGTG
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8996
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ORGANISM: Homo sapiens
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US-09-918-995-8996
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TITLE CANTENDISCON. Neith E.
TITLE OF INVENTION:
TITLE PEPLICANTION:
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2000-04-11
PRIOR PILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2038
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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; LOCATION: (51)..(293)
US-09-988-626-210
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APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, David H.F.
APPLICANT: Simard, Jacques
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APPLICANT: Simard, Jacques
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Cance and a Paralog
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT APPLICATION NUMBER: US/09/564,805
PRIOR PLING DATE: 1299-11-06
PRIOR PLING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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Pred. No. 2.7e-67;
0; Mismatches 6;
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; Sequence 210, Application US/09988687; Publication No. US20030045704A1; GENERAL INFORMATION:
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Best Local Similarity 97.7%;
Matches 251; Conservative C
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LENGTH: 350
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ORGANISM: Homo sapiens
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; LOCATION: (51)..(293)
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Mus musculus, Similar to elaC homolog 2 (E. coli), clone Encorrant Property mana.
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Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (04-FEB2-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Email: capabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NA Sequencing Center
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Result No.

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Pred. No. 0;
0; Mismatches 415; Indels 35;
                                                                                                                                                                                                         identity to protein
This clone has the following problem: frame shifted
Location/Qualifiers
                     s x.
Contact: amg@bcm.tmc.edu
dunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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81.6%; F
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Mus musculus 18 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:111003727:DNA segment, Chr 11, Wayne State
University 80, expressed, full insert seguence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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HAK004136.1 GI:12835201
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                    GAATTTCAGACCTGCCTGGTACGGCACTGCAAACATGCTTTTGGCTGCGCACTGGTACAT
                                                                                                                                                                                                                                                                                            ATGGGGAAAGATGCCACCCTCCTGATACATGAAGCCACTCTGGAGGATGGCTTGGAAGAG
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                                                                                                 1849 GTCTCCAATACTACATTGGAAAGGCTGATAAGCTTGCTGTTGGAAACATGTGACTTAGAA
                                                                                                                                  GAGTTTCAGACCTGTCTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCAC
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                                                                 1846 ATCTCCAGTCCTGCAGTGGAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAA
                                                                                                                                                                                                  1966 ACCTCTGGCTGGAAAGTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGG
                                                                                                                                                                                                                                  1969 TCATCTGGCTGGAAAGTTGTCTACTCGGGGATACCATGCCCTGTGAGGCTCTGGTCCAG
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Hayashizaki, Y.
Haya-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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TITLE RODAN, K. RODON, H. OGRARAILY, W. NERMEREN, M. And HAYASHIRAHLY, N. PREPARE FILL-Length COME TO DEPROME CHILL-Length CON 1100. 1811-510 (2000)

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                                                                                                                                                                                                               /clone lib="RIKEN full-length enriched mouse cDNA library"
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GKDATLLIHEATLEDGLEBEAVEKTHSTTSQAINVGMRMNAEFIMLNHFSQRYAKIPL
FSPDFNEKVGIAFDHMKVCFGDFPTVPKLIPPLKALFAGDIEEMVERREKRELRLVRA
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Pred. No. 1.1e-224;
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                                                                                                                                     'organism="Mus musculus"
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Best Local Similarity 83.7
Matches 1051; Conservative
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Homo sapiens cDNA clone IMAGE:5804032
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AUTHORS
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JOURNAL
COMMENT
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/clone="INAGE_1804032"
/clone="INAGE_1804032"
/closue type="IyMphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Iymph, Vector: porner, Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Size-selected >500pp for average insert size
I.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1030)

                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM2040 row: p column: 17
High quality sequence stop: 647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 908.8; DB 14; Length 1030;
Pred. No. 1.4e-222;
0; Mismatches 13; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 others
                                             NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Homo sapiens cDNA clone IMAGE:6339041
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCc
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2533 row: d column: 18
High quality sequence stop: 699.
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1. (bases 1 to 930)

NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                       541 GGCTGAAGAGCTGTGTGTTCTCTCCAGATCCTGGTGCTTTTTGTGGTGGTAGAATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                               601 AGATGAAAGCTTCATTCAACCCATCTGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAA
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rcccarcarrecrecrercaagacggaaaagcarcacrcargaaggaagagarrrr
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                                                                                                                    GGCTGAAGAGCTGTACTCCTCCAGATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCC
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AGENCOURT 8728334 NIH_MGC_47
5', mRNA sequence.
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the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies) Note: this is a NIH_MGC Library."

254 c 284 g 183 t 2 others
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                                                                                                                                                                  CTGCTACTGGACTGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAG 1593
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                                                                                                                                       1;
                                                                                                          Length 930;
                                                                                                                                       Indels
                                                                                                          Score 876; DB 14;
Pred. No. 3.6e-214;
0; Mismatches 17;
                                                                                                          35.3%;
ilarity 98.0%;
Conservative
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Matches 896; Conserv
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                                                                COUNT
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1. 918
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/ Clone lib="NIH MGC 113"
/ Llab_hoste="MHIDB (piage-resistant)"
/ Llab_hoste="MHIDB (piage-resistant)"
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/ Anote: Intervention of Sanghors.
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                                                                       mRNA linear EST 16-JUL-2002 sapiens cDNA clone IMAGE:6279815
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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High quality sequence stop: 625.
Location/Qualifiers
                                                                               bp dq
                                                                                                             AGENCOURT 8353712 NIH_MGC_113
5', mRNA Sequence
BQ706437
                                                                                                                                                                                                                                      BQ706437.1 GI:21845336
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SOURCE
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AUTHORS
TITLE
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Pred. No. 2.7e-212;
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NIH-WGC http://mgc.nci.nih.gov/.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2112 row: b column: 06
High quality sequence start: 16
High quality sequence stop: 672.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM927353 10-7 1067 bp mRNA linear EST 12-MAR-2002 AGENCOURT 6704919 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5796765 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. II (bases 1 to 1067)

II HMGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2022 row: a column: 22
High quality sequence stop: 650.
Location/Qualifiers
                                            1179
                                                                                                                                   1180 CC-GGACATCTTCCCCCTGCTCACCAGTTTCCGCT-GTAAGAAGGAGGGCCCCACCCTCA 1237
                                                                                                                                                                                                                          GTGTGCCCATGG-TTCAGGGTGAATGCCTCCAAGTACCAGGTCCGTCCCAGGA---GG 1293
                                                                                                                                                                                                                                                         GGGGCCCATGGTTTCAGGGTGAATGCCCTCCTCAGNTACAGCTCCGNTCCAANAAAGGA 989
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                                                                                                                                                             750 ACCAGCAGTGGATGGAGAAGTTTGGGCCTGACACCCCAGCACTTGGTCCTGAATGAGAACT 809
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                                                                      810 GTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTCAAACCCCCAGCTCAACCTCATCCAC
                                            GTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTCAAA-CCCAGCTCAACCTCATCCAC
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AUTHORS
TITLE
JOURNAL
COMMENT
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915 bp mRNA linear EST 16-AUG-2002
AGENCOURT 8071095 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089876
BO890505
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                               61 GCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCAATCAA 120
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GCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCAATCAA
                                                                                                         AATATTTTCTGGTCCATTGAAAGGAATAGAACTGGCTGTGCGGCCCCCACTCTGCCCCAGA
                                                                                                                                                                                                             ATACGAGGATGAAACCATGACAGTTTACCAGATCCCCATACACAGTGAACAGAGGAGGG
                                                                                                                                                                                                                                                               ATACGAGGATGAAACCATGACAGTTTACCAGATCCCCATACACAGTGAACAGAGGAGGGG
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/db xref="taxon:9606"
/dlone="MAGE.608986"
/clone=lib="MH MGC_lis"
/clone=lib="MH MGC_lis"
/tissue type="melanotic melanoma, cell line"
/tissue type="melanotic melanoma, cell line"
/tissue type="melanotic melanoma, cell line"
/lab host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: porf87; site_1: Xho1; Site_2:
ECORI; cDNA made by Oilgo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information cloud through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM2330 row: f column: 21
High quality sequence stop: 720.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 915)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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larity 99.5%; Pred. No. 1.2e-202;
Conservative 0; Mismatches 4;
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/db xref="raxxn:9606" |
/db xref="raxxn:9606" |
/clone="IMAGE:5813014" |
/clone="IMAGE:5813014" |
/clone="IMAGE:5813014" |
/clone="IMAGE:5813014" |
/clone="IMAGE:5813014" |
/clone="Organ: Iymphoma, cell line" |
/lab host="DH108 (phage-resistant)" |
/lab host="DH108 (phage-resistant)" |
/clone="Organ: Iymph; Vector: pOTB7; Site_1: XhoI; Site_2: Root="Organ: Iymph; Vector: poTB7; Site_1: XhoI; Site_2: GGCACGAG(G). Size-selected >500bp for average insert size incorrected by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) |
using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ057402 1042 bp mRNA linear EST 29-MAR-2002
AGENCOURT_6739613 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813014
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National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2064 row: f column: 23

High quality sequence stop: 663.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 5.4e-202;
); Mismatches 22; Indels 6;
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Best Local Similarity 96.9%;
Matches 868; Conservative (
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AUTHORS
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 978)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (199)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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CAGGTACCAGCAGTGGATGGAGGTTTGGGCCTGACACCCCAGCACTTGGTCCTGAATGA 1115
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                                                        GCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCAATCAA
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Library."

Tissue producents in the constraint (LLNL)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Location: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Location: MGC clone distribution information can be

http://image.llhl.gov

Location/Qualifiers

Location/Qualifiers

lucality sequence stop: 620.

Agains="Homo sapiens"

/ Clone=inforModE:592912"

/ Clone=inforModE:592912"

/ Clone=lib="NIH_MGC 99"

/ Lissue type="Iymphoma, cell line"

/ Lissue type="Iymphoma, cell line"

/ Lissue type="Iymphoma, cell priming: Directionally cloned into Ecorl Conference by oligo-dT priming: Directionally cloned into Ecorl Conference by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)

Liskb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)

Liskb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)

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Liskb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)

Liskb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)

source

FEATURES

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                                                14; Length 978
   2 others
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                                              Query Match 33.1%; Score 821.6; DB 14;
Best Local Similarity 98.5%; Pred. No. 3.7e-200;
Matches 849; Conservative 0; Mismatches 11;
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BQ064858
AGENCOURT 6856603 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929312
5, mRNA sequence.
BQ064858

BQ064858.1 GI:19893889

LOCUS DEFINITION

RESULT 10 BQ064858 human.

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Length 970

DB 14;

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Score 820.8; DB 14;
Pred. No. 6e-200;
0; Mismatches 23;
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                                 33.1%;
96.4%;
                                               Best Local Similarity 96.4
Matches 894; Conservative
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/db_xref="taxon:9606"
/dlone=IngAgE:592771"
/clone=Inje="NIH MGC 47"
/clone lib="NIH MGC 47"
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/note="organ: brain; Vector: pOTB7; Site 1: XhoI; Site_2: BCORI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size_eslected 5500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies).
Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                          970 bp mRNA linear EST 02-APR-2002
AGENCOURT 6833053 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5927571
BQ071202
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M1H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Arro
Tissue Procurement: Arro
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2102 row: I column: 04
High quality sequence stop: 723.
High quality sequence stop: 723.
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BQ069865.1 GI:19898911
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/clone="IMAGE:881525"
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/clone="IMAGE:881525"
/clone="IMAGE:881525"
/clone="IMAGE:881525"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTP7; Site_1: Xho1; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally cloned
into ECORI/Xho1 sites using the following 5' adaptor:
GGCNCGAG(6). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
// Life Technologies). Note: this is a NIH_MGC
1009 bp mRNA linear EST 29-MAR-2002
.7049753 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5815225
                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1009)
                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: agabber=remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2070 row: c column: 02
High quality sequence stop: 682.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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97.8%; Pred. No. 4.8e-195;
live 0; Mismatches 7;
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                                                                      BQ059218.1 GI:19818558
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280 c
                 AGENCOURT 7049753
5', mRNA sequence.
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BO059218
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AUTHORS
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AGENCOURT 7054570 NIH_MCC_47 Homo sapiens cDNA clone IMAGE:5922163 5', mRNA Sequence.
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/db_xref="taxon:9606"
/clone="InMGE:592163"
/clone=lib="NIH_MGC_47"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2088 row: j column: 20
High quality sequence stop: 675.
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1. (bases 1 to 983)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                   TACCAGCAGTGGATGGAGGTTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAAC
                                                                    TGTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCAC
                                                                                                                                                                                          CCGGACATCTTCCCCCTGCTCACCAGTTTCCGCTGTAAGAAGGAGGGCCCCCACCCTCAGT
                                                                                                                                                                                                                       CAGAGGGATGCCATTATTACTTGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCAACTTCCAGCAGAGCGTGCAGGAGTACAGGAGGAGTGCGCAGGAGGACGGCCCAGCCCCA
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us-09-434-382-1.rst

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4
ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/Xhol sites using the following 5' addaptor: GGCACGA(G). Size-selected 5500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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                                                                                                                                                                                 Length 983
                                                                                                                                                                                                             36; Indels
                                                                                                                                                                          Query Match
32.2%; Score 800; DB 14;
Best Local Similarity 95.2%; Pred. No. 1.4e\194;
Matches 869; Conservative 0; Mismatches 36;
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/organism="Homo sapiens"
/db xref="taxon:9606"
/dlone_"IMAGE:6210029"
/clone_"IMAGE:6210029"
/clone_type="ductal_carcinoma, cell line"
/tissue_type="ductal_carcinoma, cell line"
/note="Organ: panceras; yector: pyTB7; Site_1: XhOI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5: adaptor: GGCACGAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library." I others
                                                                                                                                                                                    876 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8039759 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6210029
5', mRNA sequence.
BQ688069
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841 GGCGACCTTCNAAGGAGAATGGAAGACCGCCAGGGAAAAACGGGAAGCTGCGGCAAGGGG 900
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1. (Dasses 1 to 876)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3370 row: column: 06
High quality sequence stop: 708.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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// Ab xref="taxon:966"
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// Clone lib="NHH MGC 112"
// Lissue_type="melanotic melanoma, cell line"
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// GGCAGGG(G). Library constructed by Ling Hong in the
// Librarory of Gerald M. Rubin (University of California,
// Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
// Superscript II RT (Life Technologies). Note: this is a
// NIH MGC Library."
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NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (WGC)

L Unpublished (1999)

Conteat: Robert Strausberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov

Tissue Proturement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLCM2492 row: n column: 13

High quality sequence stop: 615.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAAGTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCC-GGATGGGGAAAG
                                                                                                CACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCT
                                                                                                                                                                                                                                                                                                         GCTGCAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGT
                                                                                                                                                                                                                                                                                                                                                         GCTGCAGAGAGAGGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGT
                                                                                                                                                                                                   GGCTGCTGTTTGTGTCCCACCTGCACAGATCACCACACGGGCTTGCCAAGTATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -TGGAAAAGACACACAG-CACAACGTCCCAAGCCAT 2126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGAAAAGACACACAGCCACAACGTTCCAAGCCAT 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5', mRNA sequence.
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BQ679122.1 GI:21791801
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1661

300

240

1721

1781

480

1841

Homo sapiens human.

AUTHORS TITLE JOURNAL COMMENT

FEATURES

REFERENCE

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

BQ679122 LOCUS DEFINITION

841

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Gaps

1737

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        Qy
        2081 AAGAGGAAGCAGTGGAAAAGACACCACCAAACGTCCCAAGCGTGGGG--TT 2138

        Db
        781 AAAAGGAAACACATGGAAAAAACCACAGCACCAGGCCCTCANCGTGGGGGAAT 840

        Qy
        2139 GCGGATGAACCATGAGATTCATTATGC-TGAACCACTTCAG-CCAGGCCTATGCCAAGGTC 2196

        Db
        841 GCGGATGAACCAGAAGTTTTTATGCTTGAACCACTTCAGCCCACCCTATGCCAAGGGG 900

        Qy
        2197 CCCTCTTTCAGCCC 2211

        Db
        901 CCCCTTTTCAGCCC 2211

        Db
        901 CCCCTTTTCAGCCC 915

        Search completed: May 17, 2003, 18:18:07

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